GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 19:45:19 ; Search time 1184.1 Seconds
(without alignments)
10011.921 Million cell updates/sec

Title: US-09-550-163-1
Perfect score: 732
Sequence: 1 caaatccagaaaagatccgt.....atgaaaataaagccaaattt 732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	701.8	95.9	803	12	BG208163	BG208163 RST27654
	2	412.2	56.3	429	9	AI654552	AI654552 wb48b12.x
	3	393	53.7	410	9	AI962650	AI962650 wq42e03.x
	4	385.8	52.7	391	9	AI339609	AI339609 qq42a07.x
	5	372	50.8	372	9	AI246239	AI246239 qi29g04.x
c	6	301.4	41.2	350	17	AZ693989	AZ693989 AST-2HLB5
	7	295.8	40.4	1691	11	AK008619	AK008619 Mus muscu
	8	271.8	37.1	470	14	D85797	D85797 D85797 Rat
	9	256.6	35.1	1003	12	BG261965	BG261965 602373784
	10	250.8	34.3	746	12	BG221966	BG221966 RST41783
	11	241.4	33.0	252	14	BM783832	BM783832 K-EST0061
	12	188	25.7	188	9	AA633404	AA633404 np69h11.s
	13	175.4	24.0	351	13	BG938225	BG938225 lAbo14A12
	14	119.4	16.3	121	9	AA935321	AA935321 oo71g09.s
c	15	113	15.4	311	10	AW869303	AW869303 MR3-SN006
	16	101.8	13.9	314	10	BB564873	BB564873 BB564873
	17	66.2	9.0	272	10	BB574249	BB574249 BB574249
	18	61	8.3	270	10	BB595946	BB595946 BB595946
	19	57.2	7.8	358	10	BE486735	BE486735 174950 BA
	20	53.2	7.3	716	13	BI459541	BI459541 603200548
	21	52.8	7.2	464	9	AA667912	AA667912 vv19f07.r
	22	52.8	7.2	603	9	AI956381	AI956381 ul74e07.y
	23	52.8	7.2	674	10	BB613272	BB613272 BB613272
	24	52.8	7.2	754	11	AK008938	AK008938 Mus muscu
	25	51.8	7.1	311	10	AW869303	AW869303 MR3-SN006
c	26	51	7.0	424	13	BM389584	BM389584 UI-R-CN1-
c	27	51	7.0	760	14	BQ194830	BQ194830 UI-R-CN1-
	28	50.8	6.9	869	12	BF540248	BF540248 602050296
	29	45.6	6.2	986	17	CNS076KL	AL431515 T3 end of
	30	42.2	5.8	484	13	BJ059218	BJ059218 BJ059218
c	31	42.2	5.8	687	13	BJ098508	BJ098508 BJ098508
	32	42	5.7	597	13	BJ038615	BJ038615 BJ038615
	33	40.4	5.5	589	13	BJ094875	BJ094875 BJ094875
	34	40.4	5.5	629	13	BJ095114	BJ095114 BJ095114
	35	40.4	5.5	893	14	BQ734561	BQ734561 AGENCOURT
	36	39.8	5.4	309	13	BJ059046	BJ059046 BJ059046
	37	39.8	5.4	1101	17	CNS00H80	AL073048 Drosophil
c	38	39.4	5.4	713	10	AV401298	AV401298 AV401298
	39	39	5.3	552	17	AQ855211	AQ855211 CpG1835A
c	40	39	5.3	1024	17	CNS005BT	AL058090 Drosophil
c	41	38.4	5.2	634	10	AW187570	AW187570 BNLGHi777
	42	38.4	5.2	694	12	BF479357	BF479357 L48-3026T
	43	38.4	5.2	697	13	BM301804	BM301804 MCA045A01
c	44	38.2	5.2	905	17	CNS00KHX	AL077798 Drosophil
	45	37.8	5.2	433	9	AI078277	AI078277 oz29g05.x

ALIGNMENTS

RESULT 1
BG208163/c
LOCUS BG208163 803 bp mRNA linear EST 21-APR-2001
DEFINITION RST27654 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG208163
VERSION BG208163.1 GI:13729850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 550.
FEATURES Location/Qualifiers

```
     source          1. .803
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      222 a    172 c    171 g    238 t
ORIGIN

  Query Match           95.9%;  Score 701.8;  DB 12;  Length 803;
  Best Local Similarity  98.2%;  Pred. No. 6.9e-188;
  Matches  720;  Conservative    0;  Mismatches   12;  Indels    1;  Gaps    1;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
             ||| |||||||||| || ||||||||||||||||||  |||||| ||||||||||||
Db     761 CAATTCCAGAAAAGTTCTGTTTTCCTAACCTTGTTCGCGAATTTTAATATTTAAATTGCA 702

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     701 GCAGGAGGAAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 642

Qy     121 -AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGG 179
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     641 AAAGGATTTTTATTACTTATATGTACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGG 582

Qy     180 CCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGA 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     581 CCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGA 522

Qy     240 TGGTTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGA 299
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     521 TGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCATGA 462

Qy     300 GACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGT 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     461 GACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGT 402

Qy     360 ACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     401 ACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTG 342

Qy     420 CGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 CGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGT 282

Qy     480 CCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAA 539
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     281 CCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTAGCTTAGAAGAA 222

Qy     540 AGTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAG 599
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     221 AGTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAG 162

Qy     600 ATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTG 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 ATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTG 102

Qy     660 AAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAA 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 AAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAA 42

Qy     720 TAAAGCCAAATTT 732
           || |||||||||| .
Db      41 TAGAGCCAAATTT 29


RESULT 2
AI654552
```

```
LOCUS       AI654552               429 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wb48b12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308895 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI654552
VERSION     AI654552.1  GI:4738531
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 771   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2308895"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      127 a    100 c     97 g    104 t      1 others
ORIGIN

  Query Match           56.3%;  Score 412.2;  DB 9;  Length 429;
  Best Local Similarity  99.0%;  Pred. No. 7.1e-106;
  Matches  414;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     110 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 71

Qy     170 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 131

Qy     230 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 191

Qy     290 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 251

Qy     350 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 409
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 311
```

```
Qy    410 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAA 469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAA 371

Qy    470 CATCTGACGTCCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTT 527
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 CATNCTGCGTCCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTT 429


RESULT 3
AI962650
LOCUS       AI962650                410 bp    mRNA    linear   EST 08-MAR-2000
DEFINITION  wq42e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473948 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI962650
VERSION     AI962650.1  GI:5755363
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 770   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2473948"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT      120 a     93 c     93 g    104 t
ORIGIN

  Query Match             53.7%;  Score 393;  DB 9;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-100;
  Matches  393;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    110 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     18 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 77

Qy    170 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 137

Qy    230 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 197

Qy    290 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 257

Qy    350 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 317

Qy    410 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAA 469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAA 377

Qy    470 CATCTGACGTCCAGACATGAAGAGATGCCAGTG 502
          |||||||||||||||||||||||||||||||||
Db    378 CATCTGACGTCCAGACATGAAGAGATGCCAGTG 410


RESULT 4
AI339609
LOCUS       AI339609                391 bp    mRNA    linear   EST 29-DEC-1998
DEFINITION  qq42a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935156
            3' similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI339609
VERSION     AI339609.1  GI:4076536
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1935156"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      119 a     93 c     93 g     86 t
ORIGIN

  Query Match             52.7%;  Score 385.8;  DB 9;  Length 391;
  Best Local Similarity   99.5%;  Pred. No. 2.1e-98;
  Matches  387;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    111 ACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTG 170
```

```
          ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db      3 ACGTCTTCCGAAGGATTTTTATTACTTATGGGGACAATTGGCGCCAGAACACAACAGCTG 62

Qy    171 AGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACC 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 AGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACC 122

Qy    231 TCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGA 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 TCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGA 182

Qy    291 AATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGC 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 AATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGC 242

Qy    351 AGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    243 AGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGA 302

Qy    411 ACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAAC 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    303 ACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAAC 362

Qy    471 ATCTGACGTCCAGACATGAAGAGATGCCA 499
          |||||||||||||||||||||||||||||
Db    363 ATCTGACGTCCAGACATGAAGAGATGCCA 391


RESULT 5
AI246239
LOCUS       AI246239                372 bp    mRNA    linear   EST 28-JAN-1999
DEFINITION  qi29g04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857942
            3' similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI246239
VERSION     AI246239.1  GI:3841636
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 921   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 365.
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1857942"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."

BASE COUNT      115 a     89 c     86 g     82 t
ORIGIN

  Query Match           50.8%;  Score 372;  DB 9;  Length 372;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-94;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    118 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 60

Qy    178 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT 237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT 120

Qy    238 GATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 180

Qy    298 GAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAA 357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAA 240

Qy    358 GTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGG 417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGG 300

Qy    418 TGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGAC 477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGAC 360

Qy    478 GTCCAGACATGA 489
          ||||||||||||
Db    361 GTCCAGACATGA 372


RESULT 6
AZ693989/c
LOCUS       AZ693989                350 bp    DNA     linear   GSS 18-DEC-2000
DEFINITION  AST-2HLB5094 Genetrap HL-60 Human Promyelocytic Leukemia Library
            Homo sapiens genomic 5', DNA sequence.
ACCESSION   AZ693989
VERSION     AZ693989.1  GI:11878908
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 350)
  AUTHORS   Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A.
            , Durick,K. and Pollok,B.
  TITLE     Exon-trap tags from a HL-60 GenomeScreen(TM) Library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Greg Henkel
            Gene Expression
            Aurora Biosciences Corp.
            11010 Torreyana Road, San Diego, CA 92121, USA
            Tel: 8584048436
            Fax: 8584046719
            Email: henkelg@aurorabio.com
            Pools of cells were isolated from a GenomeScreen(TM) library. The
            library of cells was generated by retroviral integration of a gene
            tagging element consisting of: 1) A promoterless beta-lactamase
            proceeded by a splice acceptor as a reporter for gene expression;
            2) A promoter driving neomycin resistance followed by a splice
            donor to trap downstream exons. 3' RACE from neomycin gene was
            performed using total RNA from isolated pools. Output was shotgun
            cloned in pAmp-1 and used to transform DH5-alpha competent
            bacteria. 5' ends of reported sequences were immediately preceded
            by splice donor from the trapping construct.
            Class: exon-trapped.
FEATURES             Location/Qualifiers
     source          1. .350
```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Genetrap HL-60 Human Promyelocytic Leukemia Library"
/tissue_type="acute promyelocytic leukemia"
/cell_type="promyeloblast"
/cell_line="HL-60"
/note="Organ: peripheral blood; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."
BASE COUNT 103 a 84 c 59 g 104 t
ORIGIN

Query Match 41.2%; Score 301.4; DB 17; Length 350;
Best Local Similarity 99.1%; Pred. No. 1.7e-74;
Matches 324; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Qy    408 AGAACATTGGTGC-GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGC 466
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    350 AGAACATTGGTGCGGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGC 291

Qy    467 -TAACATCTGACGTCCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTC 525
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 TTAACATCTGACGTCCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTC 231

Qy    526 TTTGCTTAGAAGAAAGTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTG 585
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    230 TTTGCTTAGAAGAAAGTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTG 171

Qy    586 GTTGGCCAATAAAGATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGC 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    170 GTTGGCCAATAAAGATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGC 111

Qy    646 AATATTTTGTGCTGAAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAAT 705
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110 AATATTTTGTGCTGAAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAAT 51

Qy    706 ATCAATGATGAAAATAAAGCCAAATTT 732
          |||||||||||||||||||||||||||
Db     50 ATCAATGATGAAAATAAAGCCAAATTT 24
```

RESULT 7
AK008619
LOCUS AK008619 1691 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2200002I16:homolog to MINIMUM POTASSIUM ION CHANNEL-RELATED PEPTIDE 1 (MIRP1) (MINK-RELATED PEPTIDE 1), full insert sequence.
ACCESSION AK008619
VERSION AK008619.1 GI:12842913
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2200002I16.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5 (bases 1 to 1691)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

```
FEATURES             Location/Qualifiers
     source          1. .1691
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:2200002I16"
                     /db_xref="MGD:MGI:1901204"
                     /db_xref="taxon:10090"
                     /clone="2200002I16"
                     /sex="male"
                     /tissue_type="stomach"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             149. .520
                     /note="data source:SPTR, source key:Q9WTW0, evidence:ISS
                     homolog to MINIMUM POTASSIUM ION CHANNEL-RELATED PEPTIDE 1
                     (MIRP1) (MINK-RELATED PEPTIDE 1)
                     putative"
                     /codon_start=1
                     /protein_id="BAB25781.1"
                     /db_xref="GI:12842914"
                     /db_xref="MGD:MGI:1916393"
                     /translation="MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAE
                     NFYYVILYLMVMIGMFSFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQEKYKSQILH
                     LEDSKATIHENMGATGFTVSP"
     polyA_signal    1673. .1678
                     /note="putative"
     polyA_site      1691
                     /note="putative"
BASE COUNT      482 a    365 c    410 g    434 t
ORIGIN

  Query Match             40.4%;  Score 295.8;  DB 11;  Length 1691;
  Best Local Similarity   69.2%;  Pred. No. 1.4e-72;
  Matches  467;  Conservative    0;  Mismatches  167;  Indels   41;  Gaps    3;

Qy      59 CAGCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTC 118
           ||||| | |||||||||| | || ||| ||||||| || ||||| ||||| || | ||||
Db     134 CAGCAAGGGGGAAGCATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTC 193

Qy     119 CGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAG 178
             || ||||||||||||||||||||||||  ||| |   |||||| ||||| ||| |  ||
Db     194 AAAAAGATTTTTATTACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAG 253

Qy     179 GCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTG 238
           || ||||| |||| ||| ||||| |||||||||||||| ||||||||||||||||||||||
Db     254 GCACTCCAGGCCAGAGTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTG 313

Qy     239 ATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAG 298
           ||||| || |||||||| |||||| | |||||||||||||||||||| ||||| || |||
Db     314 ATGATCGGCATGTTCTCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAG 373

Qy     299 AGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAG 358
           | || || |||||| | ||||| |||||||||||||| || || || ||||||||||||
Db     374 CGGCGAGAGCACTCCCAGGACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAG 433

Qy     359 TACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGT 418
           ||||| || || ||| || |||| ||||| || ||||||||||||||||||||||| ||
Db     434 TACAAAAGTCAGATCCTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACATGGGG 493

Qy     419 GCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACG 478
           ||| | ||||||| | |||| |||||||     || || |                  ||
Db     494 GCGACGGGGTTCACAGTGTCACCCTGATTGATAAGGAATGGGGGCC-----------CG 541

Qy     479 TCCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGA 538
           ||  |    ||   | |||   |||  |   |  |  || | ||||  ||||| ||||||
Db     542 TCTGGCTCAGACAGGGTGCTTCTGCTGCCTCGAGAGCCCCACTTGTGCTTGCTCAGAAGA 601

Qy     539 AAGTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAA 598
           ||  |||||||   |      ||             | |
Db     602 CAGCTAGTTCCTCTGTGCAGCCTGGCTGGCAGTTGACACAG------------------- 642

Qy     599 GATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCT 658
                ||||||||| |||||||| |||| |   || |||||| |  ||| ||| ||||
```

```
Db     643 ------TGACATTTCTATCTCAGTGGTTTAGGTGAGCCTGTTGGGGTGATACTTTATGCT 696

Qy     659 GAAGACCTCTTTT----ACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGAT 714
           | || |||||||      | |   |  | || | ||| ||||||| |||| ||||| ||
Db     697 AAGGATCTCTTTTTTCACATGTTATGCAATGTAACTGTTATTTTAAACAATTTCAATCAT 756

Qy     715 GAAAATAAAGCCAAA 729
           || || | || ||||
Db     757 GAGAACAGAGGCAAA 771


RESULT 8
D85797
LOCUS       D85797                   470 bp    mRNA    linear   EST 09-SEP-1996
DEFINITION  D85797 Rat 21 day old female ovary mRNA PMSG 3h Rattus norvegicus
            cDNA, mRNA sequence.
ACCESSION   D85797
VERSION     D85797.1  GI:1469812
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 470)
  AUTHORS   Miyamoto,K., Mizutani,T., Numata,Y. and Okada,T.
  TITLE     Rat 21 day old female ovary mRNA
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Miyamoto,K.
            Institute for Molecular and Cellular Reg
            Gunma Univ., Biosignal Research Center
            Shouwa machi 3-39-15, Maebashi, Gunma 371, Japan
            Email: tmizu@sb.gunma-u.ac.jp
            5'-59.
FEATURES             Location/Qualifiers
     source          1. .470
                     /organism="Rattus norvegicus"
                     /strain="Wistar"
                     /db_xref="taxon:10116"
                     /clone_lib="Rat 21 day old female ovary mRNA PMSG 3h"
                     /sex="female"
                     /tissue_type="ovary"
                     /dev_stage="21 day old"
                     /note="tissue_type=hypothalamus; dev_stage=adult rat"
BASE COUNT      116 a    127 c    128 g     95 t      4 others
ORIGIN

  Query Match             37.1%;  Score 271.8;  DB 14;  Length 470;
  Best Local Similarity   80.6%;  Pred. No. 5e-66;
  Matches  315;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      62 CAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGA 121
           || | ||||| |||| | |||||| |||| || || ||||| ||||| || | |||| |
Db      25 CAAGGGGGAAACATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAA 84

Qy     122 AGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCC 181
           | | |||| |||||||||||||||  ||| |   |||||||||||| || ||| ||||
Db      85 AAGGTTTTCATTACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCG 144

Qy     182 CTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATG 241
           ||||| |||| ||| ||||| |||||||||||||| ||||||||||||||||||||||||
Db     145 CTCCAGGCCAGAGTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATG 204

Qy     242 ATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGA 301
           || || |||||| | |||||| | |||||||||||||||||||| ||||| || ||| |
Db     205 ATCGGCATGTTCGCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGG 264

Qy     302 CGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTAC 361
           ||||| |||||| | ||||| |||||||||| | | || ||||| |||||| | |||||
Db     265 CGGGAGCACTCCCAGGACCCGTACCACCAGTNCNTCGTGGAGGATTGGCAGCAGAAGTAT 324

Qy     362 AAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCG 421
           | ||| || |||| | |||| ||||| || ||||||| |||||||| ||| | || |||
```

```
Db    325 AGGAGTCAGATCTNGCATCTGGAAGACTCCAAGGCCATCATCCATGATAACCTGGGGGCG 384

Qy    422 GCTGGGTTCAAAATGTCCCCCTGATAAGGGA 452
          | ||||||| | |||| ||||||||| | |
Db    385 ACGGGGTTCACANTGTCACCCTGATAAAGAA 415


RESULT 9
BG261965
LOCUS       BG261965               1003 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  602373784F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481325 5',
            mRNA sequence.
ACCESSION   BG261965
VERSION     BG261965.1  GI:12771781
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10316  row: g  column: 22
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .1003
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4481325"
                     /clone_lib="NIH_MGC_94"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      249 a    218 c    302 g    234 t
ORIGIN

  Query Match             35.1%;  Score 256.6;  DB 12;  Length 1003;
  Best Local Similarity   80.8%;  Pred. No. 1.5e-61;
  Matches  324;  Conservative    0;  Mismatches   74;  Indels    3;  Gaps    2;

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||| | |||||||||| | || ||| ||||||| || ||||| ||||| || | ||||
Db     78 GCAAGGGGGAAGCATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAA 137

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          || |||||||||||||||||||||||  ||| |   |||||| ||||| ||| |  ||||
Db    138 AAAGATTTTTATTACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGC 197

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||| |||| ||| ||||| |||||||||||||| ||||||||||||||||||||||
Db    198 ACTCCAGGCCAGAGTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGAT 257

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||| || |||||||| |||||| | |||||||||||||||||| ||||| || ||| |
Db    258 GATCGGCATGTTCTCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCG 317

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
           || || |||||| |  |||| |||||||||||||| || || || ||||||||||||||
Db    318 GCGAGAGCACTCCCAGCACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTA 377

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAA--GGCCACCATCCATGAGAACAT-TGG 417
          ||| || || ||| || |||| |||||| || ||  ||||||||||||||||||||  ||
Db    378 CAAAAGTCAGATCCTGCATCTGGAAGACTCCAAAGGGCCACCATCCATGAGAACATGGGG 437

Qy    418 TGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGG 458
          ||| | |||||||| | |||| |||||||      || || |
Db    438 GGCGACGGGGTTCACAGTGTCACCCTGATTGATAAGGAATG 478


RESULT 10
BG221966
LOCUS       BG221966               746 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST41783 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG221966
VERSION     BG221966.1  GI:13747987
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 547.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      241 a    138 c    123 g    243 t      1 others
ORIGIN

  Query Match             34.3%;  Score 250.8;  DB 12;  Length 746;
  Best Local Similarity   94.9%;  Pred. No. 5.6e-60;
  Matches  280;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 512

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 572

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||||
Db    573 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACACCAGCTGAGCAGGAGGC 632

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||| |||||||||||||||||||||||||||||||||||||| | |||  |||| |||
Db    633 CCTCC-AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCCGGACCCAATGGNGAT 691
```

```
Qy    241 GATTGGAATGTTCTCTTTCAT-CATCGTGGCCATCCTGGTGAGCACTGTGAAATC 294
          ||||||||||||||| ||| ||  || | |||||||||||| ||||||||||||||
Db    692 GATTGGAATGTTCTTTTTAATAAATGGGGGCCATCCTGGGGAGCACTGTGAAATC 746


RESULT 11
BM783832
LOCUS       BM783832                252 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0061845 S17N258215 Homo sapiens cDNA clone S17N258215-2-A12
            5', mRNA sequence.
ACCESSION   BM783832
VERSION     BM783832.1  GI:19132064
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2  row: A  column: 12
            High quality sequence stop: 252.
FEATURES             Location/Qualifiers
     source          1. .252
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S17N258215-2-A12"
                     /clone_lib="S17N258215"
                     /sex="M"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT       85 a     48 c     59 g     60 t
ORIGIN

  Query Match             33.0%;  Score 241.4;  DB 14;  Length 252;
  Best Local Similarity   99.6%;  Pred. No. 1.5e-57;
  Matches  242;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    373 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 60

Qy    433 AATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCAGACATGAAGA 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCAGACATGAAGA 120

Qy    493 GATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGTGAGTTCCTTG 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    121 GATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGTGAGTTCCTTG 180

Qy    553 CTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATAGATGACATTT 612
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATAGATGACATTT 240

Qy    613 CAA 615
          |||
Db    241 CAA 243


RESULT 12
AA633404
LOCUS       AA633404                188 bp    mRNA    linear   EST 28-OCT-1997
DEFINITION  np69h11.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1131621 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AA633404
VERSION     AA633404.1  GI:2555264
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 188)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 785   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 167.
FEATURES             Location/Qualifiers
     source          1. .188
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1131621"
                     /clone_lib="NCI_CGAP_Br2"
                     /sex="female, pooled"
                     /tissue_type="breast"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from pooled bulk
                     breast tumor tissue, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  This library is the normalized version of
                     NCI_CGAP_Br1.1. Library was constructed by Bento Soares
                     and M. Fatima Bonaldo. "
BASE COUNT       66 a     45 c     45 g     32 t
ORIGIN

  Query Match             25.7%;  Score 188;  DB 9;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-42;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    286 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 60

Qy    346 CTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCA 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db     61 CTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCA 120

Qy    406 TGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAG 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAG 180

Qy    466 CTAACATC 473
          ||||||||
Db    181 CTAACATC 188


RESULT 13
BG938225
LOCUS       BG938225                351 bp    mRNA    linear   EST 11-JUN-2001
DEFINITION  1Abo14A12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
            sequence.
ACCESSION   BG938225
VERSION     BG938225.1  GI:14337597
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
  TITLE     cDNA's from bovine abomasum tissue
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dr. Stephen Moore
            . Beef Genomics Laboratory
            Dept of AFNS, University of Alberta
            410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
            Tel: 780 492 0169
            Fax: 780 492 4265
            Email: smoore@afns.ualberta.ca
            The sequence best matches gb:AP001719 (Homo sapiens genomic DNA,
            chromosome 21q, section 63/105) in main database at high score of
            212.0 and E-value of 9e-53
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Seq primer: T3 primer
            High quality sequence stop: 351
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="Bovine Abomasum cDNA Library"
                     /sex="Two males and one female mixed"
                     /tissue_type="Gastrointestinal tissue (GIT)"
                     /cell_type="Epithelial"
                     /dev_stage="Young adult"
                     /lab_host="XL1-BlueMRF'-strain"
                     /note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
                     I; Site_2: Xho I"
BASE COUNT      104 a     89 c     76 g     82 t
ORIGIN

  Query Match            24.0%;  Score 175.4;  DB 13;  Length 351;
  Best Local Similarity  86.5%;  Pred. No. 9.5e-39;
  Matches  205;  Conservative    0;  Mismatches   31;  Indels    1;  Gaps    1;

Qy     62 CAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGA 121
          ||||| ||||  ||| | ||| |||||||| | |||||||| |||||| | |||||| |
Db    115 CAGGACGGAAATATGCCAACTCTATCCAATCTGACACAGACACTGGAATATGTCTTCAAA 174

Qy    122 AGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCC 181
          | |||||||||| ||||| ||||| || |||| |  |||||||||  | ||||||||||||
Db    175 AAGATTTTTATCACTTACATGGAAAACTGGCACAGGAACACAACGGTTGAGCAAGAGGCC 234

Qy    182 CTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATG 241
          || |||||||| |||||||||||||||||||||||||||||| ||||||| |||||||||
```

```
Db    235 CTGCAAGCCAAGGTTGATGCTGAGAACTTCTACTATGTCATCTTGTACCTTATGGTGATG 294

Qy    242 ATTGGAATGTTCTCTTT-CATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 297
          || |||||||||||||| |||||| || |||||||||||||||| ||||||||||
Db    295 ATCGGAATGTTCTCTTTCCATCATTGTAGCCATCCTGGTGAGCACGGTGAAATCCAA 351


RESULT 14
AA935321
LOCUS       AA935321                121 bp    mRNA    linear   EST 07-JUL-1998
DEFINITION  oo71g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571680 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AA935321
VERSION     AA935321.1  GI:3092478
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 121)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 763   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .121
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1571680"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       33 a     31 c     28 g     29 t
ORIGIN

  Query Match            16.3%;  Score 119.4;  DB 9;  Length 121;
  Best Local Similarity  99.2%;  Pred. No. 4.4e-23;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    226 GTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCAC 285
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      1 GTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCAACGTGGCCATCCTGGTGAGCAC 60

Qy    286 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 345
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 120

Qy    346 C 346
          |
```

```
Db    121 C 121


RESULT 15
AW869303/c
LOCUS       AW869303                311 bp    mRNA    linear   EST 22-MAY-2000
DEFINITION  MR3-SN0067-240400-006-f11 SN0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW869303
VERSION     AW869303.1  GI:8003356
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 311)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR3-SN0067-240
            400-006-f11&t3=2000-04-24&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 74.
FEATURES             Location/Qualifiers
     source          1. .311
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="SN0067"
                     /dev_stage="Adult"
                     /note="Organ: stomach_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       60 a     80 c     76 g     95 t
ORIGIN

  Query Match            15.4%;  Score 113;  DB 10;  Length 311;
  Best Local Similarity  91.6%;  Pred. No. 4.5e-21;
  Matches  131;  Conservative    0;  Mismatches   10;  Indels    2;  Gaps    1;

Qy      60 AGCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCC 119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 AGCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCC 137

Qy     120 GAAGGATTTTTATTACTTATATGGACAATTGG--CGCCAGAACACAACAGCTGAGCAAGA 177
           |||||||||||||| ||| |||||||||||| ||    | ||||||| |||||||||| |||
Db     136 GAAGGATTTTTATCACTCATATGGACAATCGGGCGCCGAGAACACGACAGCTGAGCGAGA 77

Qy     178 GGCCCTCCAAGCCAAAGTTGATG 200
           |||||||||||||| ||| |||||
Db      76 GGCCCTCCAAGCCTAAGATGATG 54
```

Search completed: May 21, 2003, 21:37:51
Job time : 1197.1 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 14:23:09 ; Search time 14 Seconds
(without alignments)
258.501 Million cell updates/sec

Title: US-09-550-163-2
Perfect score: 632
Sequence: 1 MSTLSNFTQTLEDVFRRIFI.....EESKATIHENIGAAGFKMSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	132.5	21.0	129	3	US-09-069-896-3	Sequence 3, Appli
2	132.5	21.0	129	4	US-09-135-021-78	Sequence 78, Appl
3	132.5	21.0	129	4	US-09-135-020-4	Sequence 4, Appli
4	132.5	21.0	129	4	US-09-135-010A-4	Sequence 4, Appli
5	132.5	21.0	129	4	US-09-444-871-4	Sequence 4, Appli
6	132.5	21.0	129	4	US-09-597-735-4	Sequence 4, Appli
7	132.5	21.0	129	4	US-09-444-295-4	Sequence 4, Appli
8	132.5	21.0	129	4	US-09-471-468-3	Sequence 3, Appli
9	132.5	21.0	129	4	US-09-597-732-4	Sequence 4, Appli
10	132.5	21.0	129	4	US-09-679-185-2	Sequence 2, Appli
11	132.5	21.0	132	1	US-08-118-101A-6	Sequence 6, Appli
12	128	20.3	130	3	US-09-069-896-4	Sequence 4, Appli
13	128	20.3	130	4	US-09-471-468-4	Sequence 4, Appli
14	127.5	20.2	129	4	US-09-679-185-4	Sequence 4, Appli
15	74	11.7	262	4	US-09-134-001C-5532	Sequence 5532, Ap
16	70	11.1	170	3	US-09-069-896-1	Sequence 1, Appli
17	70	11.1	170	4	US-09-471-468-1	Sequence 1, Appli
18	69	10.9	411	4	US-08-887-534A-80	Sequence 80, Appl
19	66.5	10.5	563	4	US-09-134-001C-3172	Sequence 3172, Ap
20	65.5	10.4	648	4	US-09-134-001C-5161	Sequence 5161, Ap
21	65.5	10.4	987	1	US-08-436-044-6	Sequence 6, Appli
22	65.5	10.4	987	2	US-08-436-054-6	Sequence 6, Appli
23	65.5	10.4	987	5	PCT-US95-08812-6	Sequence 6, Appli
24	65.5	10.4	1276	1	US-08-222-616-24	Sequence 24, Appl
25	65.5	10.4	1276	4	US-08-446-648-24	Sequence 24, Appl
26	65.5	10.4	1276	5	PCT-US95-04228-24	Sequence 24, Appl
27	65.5	10.4	2016	4	US-09-634-920-4	Sequence 4, Appli
28	65	10.3	1835	4	US-09-404-650-5	Sequence 5, Appli
29	65	10.3	2175	4	US-09-404-650-2	Sequence 2, Appli
30	65	10.3	2188	4	US-09-404-650-4	Sequence 4, Appli
31	64.5	10.2	970	2	US-08-673-789-7	Sequence 7, Appli
32	64.5	10.2	973	1	US-08-162-809-10	Sequence 10, Appl
33	64.5	10.2	976	4	US-09-302-812-4	Sequence 4, Appli
34	64.5	10.2	976	4	US-09-511-477-4	Sequence 4, Appli
35	64.5	10.2	976	4	US-09-511-507-4	Sequence 4, Appli
36	64	10.1	1367	2	US-08-249-687C-2	Sequence 2, Appli
37	64	10.1	1367	2	US-08-625-819-2	Sequence 2, Appli
38	64	10.1	1367	3	US-08-746-559A-2	Sequence 2, Appli
39	64	10.1	1367	4	US-08-864-641B-18	Sequence 18, Appl
40	63.5	10.0	300	4	US-09-293-549-14	Sequence 14, Appl
41	63.5	10.0	439	3	US-08-448-722A-5	Sequence 5, Appli
42	63.5	10.0	439	4	US-08-189-309B-5	Sequence 5, Appli
43	63.5	10.0	2332	1	US-08-276-594A-2	Sequence 2, Appli
44	63.5	10.0	2351	1	US-08-366-851A-2	Sequence 2, Appli
45	63.5	10.0	2351	6	5171844-2	Patent No. 5171844

ALIGNMENTS

RESULT 1
US-09-069-896-3
; Sequence 3, Application US/09069896
; Patent No. 6071720
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: DELAYED RECTIFIER POTASSIUM
; TITLE OF INVENTION: CHANNEL HOMOLOG
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,896
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0507 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 452497
US-09-069-896-3

Query Match 21.0%; Score 132.5; DB 3; Length 129;

Best Local Similarity 45.1%; Pred. No. 9.3e-08;
Matches 23; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

```
Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95
```

RESULT 2
US-09-135-021-78
; Sequence 78, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-021-78

Query Match 21.0%; Score 132.5; DB 4; Length 129;
Best Local Similarity 45.1%; Pred. No. 9.3e-08;
Matches 23; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

```
Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95
```

RESULT 3
US-09-135-020-4
; Sequence 4, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-020-4

Query Match 21.0%; Score 132.5; DB 4; Length 129;
Best Local Similarity 45.1%; Pred. No. 9.3e-08;
Matches 23; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

```
Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95
```

RESULT 4
US-09-135-010A-4
; Sequence 4, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/135,010A
; CURRENT FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-135-010A-4

Query Match 21.0%; Score 132.5; DB 4; Length 129;
Best Local Similarity 45.1%; Pred. No. 9.3e-08;
Matches 23; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

```
Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95
```

RESULT 5
US-09-444-871-4
; Sequence 4, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22
; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114

```
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-444-871-4

  Query Match             21.0%;  Score 132.5;  DB 4;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 9.3e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 6
US-09-597-735-4
; Sequence 4, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Curran, Mark E.
;  APPLICANT: Landes, Gregory M.
;  APPLICANT: Connors, Timothy D.
;  APPLICANT: Burn, Timothy C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,735
;  CURRENT FILING DATE: 2000-06-19
;  EARLIER APPLICATION NUMBER: 09/135,010
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-597-735-4

  Query Match             21.0%;  Score 132.5;  DB 4;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 9.3e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 7
US-09-444-295-4
; Sequence 4, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,295
;  CURRENT FILING DATE:  1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-444-295-4

  Query Match             21.0%;  Score 132.5;  DB 4;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 9.3e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 8
US-09-471-468-3
; Sequence 3, Application US/09471468
; Patent No. 6432687
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Patterson, Chandra
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DELAYED RECTIFIER POTASSIUM
;    TITLE OF INVENTION:  CHANNEL HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/471,468
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/069,896
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0507 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
```

```
;      CLONE:  452497
US-09-471-468-3

  Query Match             21.0%;  Score 132.5;  DB 4;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 9.3e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: |||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 9
US-09-597-732-4
; Sequence 4, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,732
;  CURRENT FILING DATE:  2000-06-19
;  PRIOR APPLICATION NUMBER: 09/135,010
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-597-732-4

  Query Match             21.0%;  Score 132.5;  DB 4;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 9.3e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: |||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 10
US-09-679-185-2
; Sequence 2, Application US/09679185
; Patent No. 6458542
; GENERAL INFORMATION:
;  APPLICANT: George Jr., Alfred L.
;  APPLICANT:  Roden, Dan M
;  TITLE OF INVENTION: METHOD OF SCREENING FOR SUSCEPTIBILITY TO
;  TITLE OF INVENTION:  DRUG-INDUCED CARDIAC ARRYTHMIA
;  FILE REFERENCE: Attorney Docket No. 6458542 1242-33-2
;  CURRENT APPLICATION NUMBER: US/09/679,185
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 60/158,696
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-679-185-2

  Query Match             21.0%;  Score 132.5;  DB 4;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 9.3e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: |||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 11
US-08-118-101A-6
; Sequence 6, Application US/08118101A
; Patent No. 5620892
;  GENERAL INFORMATION:
;    APPLICANT:  Kurtz, Stephen E.
;    APPLICANT:  Knickerbocker, Aron M.
;    APPLICANT:  McCullough, John R.
;    TITLE OF INVENTION:  A STRAIN OF SACCHAROMYCES CEREVISIAE
;    TITLE OF INVENTION:  EXPRESSING THE GENE ENCODING POTASSIUM TRANSPORTER MINK
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burton Rodney
;      STREET:  P.O. Box 4000
;      CITY:  Princeton
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  08543-4000
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,101A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaul, Timothy J.
;      REGISTRATION NUMBER:  33,111
;      REFERENCE/DOCKET NUMBER:  DC27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 252-5901
;      TELEFAX:  (609) 252-4526
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  132 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-118-101A-6

  Query Match             21.0%;  Score 132.5;  DB 1;  Length 132;
  Best Local Similarity   45.1%;  Pred. No. 9.6e-08;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: |||||||:: ||  | |||| |: :
Db      48 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 98


RESULT 12
US-09-069-896-4
; Sequence 4, Application US/09069896
; Patent No. 6071720
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Patterson, Chandra
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DELAYED RECTIFIER POTASSIUM
```

```
;    TITLE OF INVENTION:  CHANNEL HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,896
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0507 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  130 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  203977
US-09-069-896-4

  Query Match             20.3%;  Score 128;  DB 3;  Length 130;
  Best Local Similarity   41.4%;  Pred. No. 3e-07;
  Matches   29;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    3;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESK 107
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:  |   ||  :
Db      46 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDAWQEKGKALFQARVLESFR 105

Qy     108 AT-IHENIGA 116
           |  : ||  |
Db     106 ACYVIENQAA 115


RESULT 13
US-09-471-468-4
; Sequence 4, Application US/09471468
; Patent No. 6432687
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Patterson, Chandra
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DELAYED RECTIFIER POTASSIUM
;    TITLE OF INVENTION:  CHANNEL HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/471,468
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/069,896
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0507 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  130 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  203977
US-09-471-468-4

  Query Match             20.3%;  Score 128;  DB 4;  Length 130;
  Best Local Similarity   41.4%;  Pred. No. 3e-07;
  Matches   29;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    3;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESK 107
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:  |   ||  :
Db      46 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDAWQEKGKALFQARVLESFR 105

Qy     108 AT-IHENIGA 116
           |  : ||  |
Db     106 ACYVIENQAA 115


RESULT 14
US-09-679-185-4
; Sequence 4, Application US/09679185
; Patent No. 6458542
; GENERAL INFORMATION:
;  APPLICANT: George Jr., Alfred L.
;  APPLICANT:  Roden, Dan M
;  TITLE OF INVENTION: METHOD OF SCREENING FOR SUSCEPTIBILITY TO
;  TITLE OF INVENTION:  DRUG-INDUCED CARDIAC ARRYTHMIA
;  FILE REFERENCE: Attorney Docket No. 6458542 1242-33-2
;  CURRENT APPLICATION NUMBER: US/09/679,185
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 60/158,696
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-679-185-4

  Query Match             20.2%;  Score 127.5;  DB 4;  Length 129;
  Best Local Similarity   43.1%;  Pred. No. 3.4e-07;
  Matches   22;  Conservative   16;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  : |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESNAWQEKDKAYV 95
```

```
RESULT 15
US-09-134-001C-5532
; Sequence 5532, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5532
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5532

  Query Match             11.7%;  Score 74;  DB 4;  Length 262;
  Best Local Similarity   25.0%;  Pred. No. 0.98;
  Matches   23;  Conservative   19;  Mismatches   30;  Indels   20;  Gaps    5;

Qy      14 VFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVK 73
           :|: |:  |    ::  |   :  |        ||:|| ::::      ::| || :|:|
Db       1 IFKNIYCLY----KKGVTMRDKDNQ----HSRLYYIILTIVIIA---ICVVVVILFNTLK 49

Qy      74 SKRREHSNDPYHQYIV--------EDWQEKYK 97
           :  | || | |  :          :||: | |
Db      50 T-NRSHSTDRYADFTELKKDTIKNKDWRIKTK 80


Search completed: May 15, 2003, 14:26:32
Job time : 16 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 20:27:39 ; Search time 100.392 Seconds
(without alignments)
9628.006 Million cell updates/sec

Title: US-09-550-163-1
Perfect score: 732
Sequence: 1 caaatccagaaaagatccgt.....atgaaaataaagccaaattt 732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	730.4	99.8	732	9	US-10-000-151B-5	Sequence 5, Appli
	2	730.4	99.8	113604	9	US-10-227-195A-1	Sequence 1, Appli
	3	730.4	99.8	113604	9	US-10-227-195A-2	Sequence 2, Appli
	4	372	50.8	372	10	US-09-864-761-33139	Sequence 33139, A
	5	368	50.3	450	10	US-09-864-761-3463	Sequence 3463, Ap
	6	312	42.6	312	10	US-09-864-761-20233	Sequence 20233, A
	7	306	41.8	471	10	US-09-864-761-16671	Sequence 16671, A
c	8	53.2	7.3	231	10	US-09-864-761-20783	Sequence 20783, A
c	9	53.2	7.3	390	10	US-09-864-761-17593	Sequence 17593, A
	10	53.2	7.3	1703	9	US-10-138-316-3	Sequence 3, Appli
c	11	53.2	7.3	113604	9	US-10-227-195A-1	Sequence 1, Appli
c	12	53.2	7.3	113604	9	US-10-227-195A-2	Sequence 2, Appli
c	13	50.8	6.9	468	10	US-09-864-761-4026	Sequence 4026, Ap
c	14	46	6.3	381	10	US-09-864-761-810	Sequence 810, App
	15	36	4.9	1146	10	US-09-853-386-111	Sequence 111, App
	16	36	4.9	1206	10	US-09-853-386-107	Sequence 107, App
	17	36	4.9	1206	10	US-09-853-386-117	Sequence 117, App
	18	36	4.9	1495	10	US-09-191-724-1	Sequence 1, Appli
	19	36	4.9	1582	10	US-09-191-724-14	Sequence 14, Appl
c	20	36	4.9	2579	10	US-09-822-830A-30	Sequence 30, Appl
	21	35.8	4.9	4057	9	US-10-239-676-181	Sequence 181, App
	22	34.8	4.8	527	9	US-10-184-644-522	Sequence 522, App
	23	34.8	4.8	527	9	US-10-184-634-522	Sequence 522, App
c	24	34.8	4.8	2000	9	US-09-938-842A-4768	Sequence 4768, Ap
	25	34	4.6	123526	9	US-09-910-185-11	Sequence 11, Appl
	26	33.6	4.6	653	9	US-10-184-644-402	Sequence 402, App
	27	33.6	4.6	653	9	US-10-184-634-402	Sequence 402, App
c	28	33.6	4.6	1140	12	US-10-003-356-6	Sequence 6, Appli
c	29	33.6	4.6	2781	12	US-10-003-356-9	Sequence 9, Appli
	30	33.4	4.6	4104	9	US-09-992-598-277	Sequence 277, App
	31	33.4	4.6	4104	9	US-09-989-293A-277	Sequence 277, App
	32	33.4	4.6	4104	9	US-09-989-735-277	Sequence 277, App
	33	33.4	4.6	4104	9	US-09-990-444-277	Sequence 277, App
	34	33.4	4.6	4104	9	US-09-989-730-277	Sequence 277, App
	35	33.4	4.6	4104	9	US-09-990-436-277	Sequence 277, App
	36	33.4	4.6	4104	9	US-09-991-181-277	Sequence 277, App
	37	33.4	4.6	4104	9	US-09-993-687-277	Sequence 277, App
	38	33.4	4.6	4104	9	US-09-989-734-277	Sequence 277, App
	39	33.4	4.6	4104	9	US-10-028-072-449	Sequence 449, App
	40	33.4	4.6	4104	9	US-09-997-653-277	Sequence 277, App
	41	33.4	4.6	4104	9	US-09-993-667-277	Sequence 277, App
	42	33.4	4.6	4104	9	US-10-121-049-449	Sequence 449, App
	43	33.4	4.6	4104	9	US-10-123-904-449	Sequence 449, App
	44	33.4	4.6	4104	9	US-10-140-470-449	Sequence 449, App
	45	33.4	4.6	4104	9	US-09-990-438-277	Sequence 277, App

ALIGNMENTS

RESULT 1
US-10-000-151B-5
; Sequence 5, Application US/10000151B
; Publication No. US20030013136A1
; GENERAL INFORMATION:
; APPLICANT: Balser, Jeffrey R.
; APPLICANT: George, Alfred L.
; TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
; FILE REFERENCE: Vanderbilt Ref No. US20030013136A1 VU0120; Attorney Docket No. US2
; CURRENT APPLICATION NUMBER: US/10/000,151B
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-000-151B-5

Query Match 99.8%; Score 730.4; DB 9; Length 732;
Best Local Similarity 99.9%; Pred. No. 6.6e-215;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
```

```
Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

RESULT 2
US-10-227-195A-1
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; APPLICANT: Arnold, Deana
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 1030U1
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7175, 7204, 36973, 66372, 76921, 81512, 88727
; OTHER INFORMATION: n = G or C
US-10-227-195A-1

Query Match 99.8%; Score 730.4; DB 9; Length 113604;
Best Local Similarity 99.9%; Pred. No. 1.5e-213;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17403 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 17462

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17463 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 17522

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17523 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 17582

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17583 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 17642

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17643 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 17702

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17703 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 17762

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17763 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 17822

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17823 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 17882

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17883 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 17942

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  17943 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 18002

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18003 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 18062

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18063 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 18122

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db  18123 AAAGCCAAATTT 18134
```

RESULT 3
US-10-227-195A-2
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; APPLICANT: Arnold, Deana
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 1030U1
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
US-10-227-195A-2

Query Match 99.8%; Score 730.4; DB 9; Length 113604;
Best Local Similarity 99.9%; Pred. No. 1.5e-213;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17403 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 17462

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17463 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 17522

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17523 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 17582

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17583 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 17642

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17643 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 17702

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17703 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 17762

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17763 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 17822

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17823 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 17882

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17883 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 17942

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  17943 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 18002

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18003 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 18062

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  18063 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 18122

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db  18123 AAAGCCAAATTT 18134


RESULT 4
US-09-864-761-33139
; Sequence 33139, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33139
;   LENGTH: 372
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000120.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.67
;   OTHER INFORMATION: EST_HUMAN HIT: AI654552.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: Q9Y6J6, EVALUE 8.00e-67
;   OTHER INFORMATION: NT HIT: gi11526220, EVALUE 0.00e+00
US-09-864-761-33139

  Query Match             50.8%;  Score 372;  DB 10;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-104;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy     434 ATGTCCCCCTGA 445
           ||||||||||||
Db     361 ATGTCCCCCTGA 372


RESULT 5
US-09-864-761-3463
; Sequence 3463, Application US/09864761
; Patent No. US20020048763A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3463
;   LENGTH: 450
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000052.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.88
US-09-864-761-3463

  Query Match            50.3%;  Score 368;  DB 10;  Length 450;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-103;
  Matches  368;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     83 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 142

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    143 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 202

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    203 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 262

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 322

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 382

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    383 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 442

Qy    361 CAAGAGCC 368
          ||||||||
Db    443 CAAGAGCC 450


RESULT 6
US-09-864-761-20233
; Sequence 20233, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
```

```
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20233
;   LENGTH: 312
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000052.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.88
;   OTHER INFORMATION: EST_HUMAN HIT: AI246239.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: Q9Y6J6, EVALUE 3.00e-55
;   OTHER INFORMATION: NT HIT: AF302095.1, EVALUE 0.00e+00
US-09-864-761-20233

  Query Match             42.6%;  Score 312;  DB 10;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 5e-86;
  Matches  312;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    127 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 60

Qy    187 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120

Qy    247 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 180

Qy    307 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 240

Qy    367 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 300

Qy    427 GTTCAAAATGTC 438
          ||||||||||||
Db    301 GTTCAAAATGTC 312


RESULT 7
US-09-864-761-16671
; Sequence 16671, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16671
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000120.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.67
US-09-864-761-16671

  Query Match             41.8%;  Score 306;  DB 10;  Length 471;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-84;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 225

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 285

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 345

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 405

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 465

Qy    301 ACGGGA 306
          ||||||
Db    466 ACGGGA 471
```

```
RESULT 8
US-09-864-761-20783/c
; Sequence 20783, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20783
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000121.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
;   OTHER INFORMATION: SWISSPROT HIT: P15382, EVALUE 2.00e-39
;   OTHER INFORMATION: EST_HUMAN HIT: AW847275.1, EVALUE 5.60e-01
;   OTHER INFORMATION: NT HIT: AF135188.1, EVALUE 1.00e-127
US-09-864-761-20783

  Query Match             7.3%;  Score 53.2;  DB 10;  Length 231;
  Best Local Similarity   63.6%;  Pred. No. 3e-06;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     207 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 148

Qy     283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
           |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||  |
Db     147 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 88

Qy     340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db      87 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 54


RESULT 9
US-09-864-761-17593/c
; Sequence 17593, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17593
;   LENGTH: 390
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000168.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
```

```
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
;   OTHER INFORMATION: EST_HUMAN HIT: AA770188.1, EVALUE 6.30e-02
;   OTHER INFORMATION: SWISSPROT HIT: P15382, EVALUE 4.00e-61
;   OTHER INFORMATION: NT HIT: gi11526222, EVALUE 0.00e+00
US-09-864-761-17593

  Query Match             7.3%;  Score 53.2;  DB 10;  Length 390;
  Best Local Similarity   63.6%;  Pred. No. 4.2e-06;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    209 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 150

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    149 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 90

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db     89 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 56


RESULT 10
US-10-138-316-3
; Sequence 3, Application US/10138316
; Publication No. US20030054380A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-162
;  CURRENT APPLICATION NUMBER: US/10/138,316
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/444,295
;  PRIOR FILING DATE: 1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
;   FEATURE:
;   NAME/KEY: misc
;   LOCATION: (1)..(1703)
;   OTHER INFORMATION: n may be any nucleotide
US-10-138-316-3

  Query Match             7.3%;  Score 53.2;  DB 9;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 1e-05;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 11
US-10-227-195A-1/c
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
;  APPLICANT: Cox, David
;  APPLICANT:  Arnold, Deana
;  TITLE OF INVENTION: Haplotype structure of chromosome 21
;  FILE REFERENCE: 1030U1
;  CURRENT APPLICATION NUMBER: US/10/227,195A
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 113604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7175, 7204, 36973, 66372, 76921, 81512, 88727
;   OTHER INFORMATION: n = G or C
US-10-227-195A-1

  Query Match             7.3%;  Score 53.2;  DB 9;  Length 113604;
  Best Local Similarity   63.6%;  Pred. No. 0.00014;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db  96499 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 96440

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db  96439 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 96380

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db  96379 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 96346


RESULT 12
US-10-227-195A-2/c
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
;  APPLICANT: Cox, David
;  APPLICANT:  Arnold, Deana
;  TITLE OF INVENTION: Haplotype structure of chromosome 21
;  FILE REFERENCE: 1030U1
;  CURRENT APPLICATION NUMBER: US/10/227,195A
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 113604
;   TYPE: DNA
;   ORGANISM: Human
```

```
US-10-227-195A-2

  Query Match             7.3%;  Score 53.2;  DB 9;  Length 113604;
  Best Local Similarity   63.6%;  Pred. No. 0.00014;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db   96499 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 96440

Qy     283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
           |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db   96439 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 96380

Qy     340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db   96379 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 96346


RESULT 13
US-09-864-761-4026/c
; Sequence 4026, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4026
;   LENGTH: 468
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000121.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
US-09-864-761-4026

  Query Match             6.9%;  Score 50.8;  DB 10;  Length 468;
  Best Local Similarity   63.3%;  Pred. No. 2.6e-05;
  Matches   95;  Conservative    0;  Mismatches   52;  Indels    3;  Gaps    1;

Qy     227 TACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACT 286
           ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || |||||
Db     467 TACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAGCTAC 408

Qy     287 GTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---TAGAG 343
           |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |     ||
Db     407 ATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTCCGAT 348

Qy     344 GACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           | |||||| || ||| |||||  | |  ||
Db     347 GCCTGGCAAGAGAAGGACAAGGCCTATGTC 318


RESULT 14
US-09-864-761-810/c
; Sequence 810, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
```

```
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 810
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000168.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
US-09-864-761-810

  Query Match             6.3%;  Score 46;  DB 10;  Length 381;
  Best Local Similarity   64.2%;  Pred. No. 0.00069;
  Matches   86;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    1;

Qy    243 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 302
          | ||| | |||   ||| ||| | ||| |||| || |||||    |    |||||||  |
Db    378 TGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAGCTACATCCGCTCCAAGAAGC 319

Qy    303 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTA---GAGGACTGGCAGGAAAAGT 359
           ||| ||||| || ||||| | | ||   ||||| |     || | |||||| || |||
Db    318 TGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTCCGATGCCTGGCAAGAGAAGG 259

Qy    360 ACAAGAGCCAAATC 373
          |||||  | |  ||
Db    258 ACAAGGCCTATGTC 245


RESULT 15
US-09-853-386-111
; Sequence 111, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Evelyn
;  APPLICANT:  Bresnihan, Barry
;  APPLICANT:  Conneely, Orla
;  APPLICANT:  Fitzgerald, Oliver
;  TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
;  TITLE OF INVENTION:  Subfamily of Nuclear Transcription Factors
;  FILE REFERENCE: P01972US1
;  CURRENT APPLICATION NUMBER: US/09/853,386
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/203645
;  PRIOR FILING DATE: 2000-05-12
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
;   LENGTH: 1146
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-853-386-111

  Query Match             4.9%;  Score 36;  DB 10;  Length 1146;
  Best Local Similarity   52.7%;  Pred. No. 1.7;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy    188 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 247
          | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db    679 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 738

Qy    248 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 307
          || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db    739 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 798

Qy    308 CACTCCAATGACCCCTACCACCAGTACA 335
          | |||          |   |||||||
Db    799 TCCACCACGTCTGAGACCATTCAGTACA 826


Search completed: May 21, 2003, 22:42:03
Job time : 217.392 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 20:14:00 ; Search time 42.5504 Seconds
(without alignments)
5275.799 Million cell updates/sec

Title: US-09-550-163-1
Perfect score: 732
Sequence: 1 caaatccagaaaagatccgt.....atgaaaataaagccaaattt 732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53.2	7.3	398	1	US-08-118-101A-5	Sequence 5, Appli
2	53.2	7.3	436	4	US-09-679-185-1	Sequence 1, Appli
3	53.2	7.3	1703	3	US-09-135-021-77	Sequence 77, Appl
4	53.2	7.3	1703	4	US-09-135-020-3	Sequence 3, Appli
5	53.2	7.3	1703	4	US-09-135-010A-3	Sequence 3, Appli
6	53.2	7.3	1703	4	US-09-444-871-3	Sequence 3, Appli
7	53.2	7.3	1703	4	US-09-597-735-3	Sequence 3, Appli
8	53.2	7.3	1703	4	US-09-444-295-3	Sequence 3, Appli
9	53.2	7.3	1703	4	US-09-597-732-3	Sequence 3, Appli
10	51.6	7.0	436	4	US-09-679-185-3	Sequence 3, Appli
11	36.6	5.0	2652	1	US-08-318-831-1	Sequence 1, Appli
c 12	36.2	4.9	7218	1	US-08-232-463-14	Sequence 14, Appl
13	36	4.9	1380	1	US-08-110-286A-1	Sequence 1, Appli
14	36	4.9	1495	4	US-08-482-746-1	Sequence 1, Appli
15	36	4.9	1582	4	US-08-482-746-14	Sequence 14, Appl
16	33.6	4.6	645	3	US-09-069-896-2	Sequence 2, Appli
17	33.6	4.6	645	4	US-09-471-468-2	Sequence 2, Appli
18	33	4.5	606	4	US-09-328-111-133	Sequence 133, App
c 19	33	4.5	2912	4	US-09-307-143-3	Sequence 3, Appli
c 20	32.4	4.4	837	4	US-08-998-416-303	Sequence 303, App
c 21	32.4	4.4	4659	4	US-09-221-017B-823	Sequence 823, App
22	32.2	4.4	43676	3	US-09-356-952-12	Sequence 12, Appl
23	32	4.4	246240	2	US-08-724-394A-20	Sequence 20, Appl
24	32	4.4	246240	2	US-08-724-394A-21	Sequence 21, Appl
25	32	4.4	246240	2	US-08-724-394A-22	Sequence 22, Appl
c 26	31.4	4.3	566	4	US-09-221-017B-919	Sequence 919, App
c 27	30.6	4.2	744	3	US-08-969-644-17	Sequence 17, Appl
c 28	30.6	4.2	744	3	US-08-444-189-17	Sequence 17, Appl
c 29	30.6	4.2	744	4	US-08-468-544-17	Sequence 17, Appl
c 30	30.6	4.2	2929	4	US-09-705-299-10	Sequence 10, Appl
31	30.6	4.2	6822	4	US-09-426-998-3	Sequence 3, Appli
c 32	30.6	4.2	7502	3	US-08-969-644-6	Sequence 6, Appli
c 33	30.6	4.2	7502	3	US-08-444-189-6	Sequence 6, Appli
c 34	30.6	4.2	7502	4	US-08-468-544-6	Sequence 6, Appli
35	30.6	4.2	7741	4	US-09-426-998-4	Sequence 4, Appli
c 36	30.6	4.2	98844	4	US-09-791-211-10	Sequence 10, Appl
c 37	30.4	4.2	28473	4	US-08-961-527-83	Sequence 83, Appl
38	30.2	4.1	28001	4	US-09-819-993-3	Sequence 3, Appli
39	30.2	4.1	33000	4	US-09-215-694-18	Sequence 18, Appl
40	30	4.1	1001	4	US-09-641-638-198	Sequence 198, App
c 41	29.8	4.1	2266	2	US-08-724-394A-18	Sequence 18, Appl
42	29.8	4.1	72604	4	US-09-268-992-7	Sequence 7, Appli
43	29.8	4.1	72604	4	US-09-657-474-7	Sequence 7, Appli
44	29.6	4.0	462	3	US-08-863-813A-33	Sequence 33, Appl
45	29.6	4.0	3273	6	5516630-1	Patent No. 5516630

ALIGNMENTS

```
RESULT 1
US-08-118-101A-5
; Sequence 5, Application US/08118101A
; Patent No. 5620892
;  GENERAL INFORMATION:
;    APPLICANT:  Kurtz, Stephen E.
;    APPLICANT:  Knickerbocker, Aron M.
;    APPLICANT:  McCullough, John R.
;    TITLE OF INVENTION:  A STRAIN OF SACCHAROMYCES CEREVISIAE
;    TITLE OF INVENTION:  EXPRESSING THE GENE ENCODING POTASSIUM TRANSPORTER MINK
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burton Rodney
;      STREET:  P.O. Box 4000
;      CITY:  Princeton
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  08543-4000
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,101A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaul, Timothy J.
;      REGISTRATION NUMBER:  33,111
;      REFERENCE/DOCKET NUMBER:  DC27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 252-5901
;      TELEFAX:  (609) 252-4526
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  398 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..398
US-08-118-101A-5

  Query Match             7.3%;  Score 53.2;  DB 1;  Length 398;
  Best Local Similarity   63.6%;  Pred. No. 3.4e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;
```

```
Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    141 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 200

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    201 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 260

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
          || | |||||| || ||| |||||  | |  ||
Db    261 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 294


RESULT 2
US-09-679-185-1
; Sequence 1, Application US/09679185
; Patent No. 6458542
; GENERAL INFORMATION:
;  APPLICANT: George Jr., Alfred L.
;  APPLICANT:  Roden, Dan M
;  TITLE OF INVENTION: METHOD OF SCREENING FOR SUSCEPTIBILITY TO
;  TITLE OF INVENTION:  DRUG-INDUCED CARDIAC ARRYTHMIA
;  FILE REFERENCE: Attorney Docket No. 6458542 1242-33-2
;  CURRENT APPLICATION NUMBER: US/09/679,185
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 60/158,696
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(418)
;  PUBLICATION INFORMATION:
;   JOURNAL: Biochem. Biophys. Res. Commun.
;   VOLUME: 161
;   PAGES: 176-181
;   DATE: May-1989
;   DATABASE ACCESSION NUMBER: GenBank M26685
;   DATABASE ENTRY DATE: 1994-03-30
US-09-679-185-1

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 436;
  Best Local Similarity   63.6%;  Pred. No. 3.6e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    160 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 219

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    220 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 279

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
          || | |||||| || ||| |||||  | |  ||
Db    280 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 313


RESULT 3
US-09-135-021-77
; Sequence 77, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-021-77

  Query Match             7.3%;  Score 53.2;  DB 3;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
          || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 4
US-09-135-020-3
; Sequence 3, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/135,020
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-020-3

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383
```

```
Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 5
US-09-135-010A-3
; Sequence 3, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
;  APPLICANT:  Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION:  KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE:  2323-133
;  CURRENT APPLICATION NUMBER: US/09/135,010A
;  CURRENT FILING DATE:  1998-08-17
;  PRIOR APPLICATION NUMBER:  60/094,477
;  PRIOR FILING DATE:  1998-07-29
;  PRIOR APPLICATION NUMBER:  08/921,068
;  PRIOR FILING DATE:  1997-08-29
;  PRIOR APPLICATION NUMBER:  08/739,383
;  PRIOR FILING DATE:  1996-10-29
;  PRIOR APPLICATION NUMBER:  60/019,014
;  PRIOR FILING DATE:  1995-12-22
;  NUMBER OF SEQ ID NOS:  116
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-010A-3

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 6
US-09-444-871-3
; Sequence 3, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,871
;  CURRENT FILING DATE: 1999-11-22
;  EARLIER APPLICATION NUMBER: US 09/135,020
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-444-871-3

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 7
US-09-597-735-3
; Sequence 3, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Curran, Mark E.
;  APPLICANT: Landes, Gregory M.
;  APPLICANT: Connors, Timothy D.
;  APPLICANT: Burn, Timothy C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,735
;  CURRENT FILING DATE: 2000-06-19
;  EARLIER APPLICATION NUMBER: 09/135,010
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-597-735-3

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 8
US-09-444-295-3
; Sequence 3, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,295
;  CURRENT FILING DATE:  1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-444-295-3

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 9
US-09-597-732-3
; Sequence 3, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,732
;  CURRENT FILING DATE:  2000-06-19
;  PRIOR APPLICATION NUMBER: 09/135,010
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-597-732-3

  Query Match             7.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 7.7e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 10
US-09-679-185-3
; Sequence 3, Application US/09679185
; Patent No. 6458542
; GENERAL INFORMATION:
;  APPLICANT: George Jr., Alfred L.
;  APPLICANT:  Roden, Dan M
;  TITLE OF INVENTION: METHOD OF SCREENING FOR SUSCEPTIBILITY TO
;  TITLE OF INVENTION:  DRUG-INDUCED CARDIAC ARRYTHMIA
;  FILE REFERENCE: Attorney Docket No. 6458542 1242-33-2
;  CURRENT APPLICATION NUMBER: US/09/679,185
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 60/158,696
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 436
```

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(418)
US-09-679-185-3

  Query Match             7.0%;  Score 51.6;  DB 4;  Length 436;
  Best Local Similarity   63.0%;  Pred. No. 1.1e-06;
  Matches   97;  Conservative    0;  Mismatches   54;  Indels    3;  Gaps    1;

Qy     223 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 282
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     160 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 219

Qy     283 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 339
           |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db     220 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 279

Qy     340 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373
           | | |||||| || ||| |||||  | |  ||
Db     280 CAATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 313


RESULT 11
US-08-318-831-1
; Sequence 1, Application US/08318831
; Patent No. 5656595
;  GENERAL INFORMATION:
;    APPLICANT:  Schweighoffer, Fabien
;    APPLICANT:  Tocque, Bruno
;    TITLE OF INVENTION:  PEPTIDES HAVING A GDP EXCHANGE FACTOR
;    TITLE OF INVENTION:  ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES,
;    TITLE OF INVENTION:  PREPARATION AND UTILIZATION
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.1 (EPO Patentin)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,831
;      FILING DATE:  19 October 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR92/04827
;      FILING DATE:  21-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, Julie K.
;      REGISTRATION NUMBER:  P-38,619
;      REFERENCE/DOCKET NUMBER:  ST92033-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2652 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2445
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  445..2445 (SEQ ID NO 3)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  976..2445 (SEQ ID NO 4)
US-08-318-831-1

  Query Match             5.0%;  Score 36.6;  DB 1;  Length 2652;
  Best Local Similarity   53.1%;  Pred. No. 0.17;
  Matches   78;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy     128 TTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAA 187
           | ||  | |  | |   | | | |  ||| ||| |  || ||||    | | ||  || |
Db    2402 TCTACGAGTCTTCTCTCCGAATAGAACCAAAACTCCCCACCTGAAGCTGTGCCCAGCCCA 2461

Qy     188 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 247
           | |  || || | | | | || | | |||  | || ||||||  |  | ||   | ||
Db    2462 GACCCAGCTGCTCCCGGGGACATGTGCTAGATGATACTGTACATATTCGTTTGGTTTCAC 2521

Qy     248 ATGTTCTCTTTCATCATCGTGGCCATC 274
           | | |  ||| |||   ||  | ||
Db    2522 TGGATTTTCTTCTTCAGTATGTGCTTC 2548


RESULT 12
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14
```

```
  Query Match             4.9%;  Score 36.2;  DB 1;  Length 7218;
  Best Local Similarity   2.3%;  Pred. No. 0.4;
  Matches    8;  Conservative  191;  Mismatches  144;  Indels    0;  Gaps    0;

Qy     277 GGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACAT 336
           :: ::: :  : ::::   :::::: ::::: :    :: ::      :  :  :: : :
Db    1398 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1339

Qy     337 TGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGC 396
           : ::::::  :: :::::::: : :::::  :::    :::   ::::::  :::::
Db    1338 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1279

Qy     397 CACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAA 456
           :  :   : ::::: :  :: : ::  :::   :::: :       :: ::::::::::
Db    1278 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1219

Qy     457 GGCACCAAGCTAACATCTGACGTCCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATC 516
           :: :  :::  :: :   :: :   ::: : ::::::: :  :: :  : :::: :::
Db    1218 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1159

Qy     517 CAAATTGTCTTTGCTTAGAAGAAAGTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGA 576
           :::  :     :   ::::::::: :::      :      :  :::::     : :::
Db    1158 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1099

Qy     577 GATTATGTGGTTGGCCAATAAAGATAGATGACATTTCAATCTC 619
           ::  : : ::  ::  :: ::::: ::: :: ||  ||| |||
Db    1098 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTC 1056


RESULT 13
US-08-110-286A-1
; Sequence 1, Application US/08110286A
; Patent No. 5728545
;  GENERAL INFORMATION:
;    APPLICANT:  Perrin, Marilyn H.
;    APPLICANT:  Chen, Ruoping
;    APPLICANT:  Lewis, Kathy A.
;    APPLICANT:  Vale Jr., Wylie W.
;    APPLICANT:  Donaldson, Cynthia J.
;    TITLE OF INVENTION:  CLONING AND RECOMBINANT PRODUCTION OF
;    TITLE OF INVENTION:  CRF RECEPTOR(S)
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pretty, Schroeder, Brueggemann & Clark
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/110,286A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/079,320
;      FILING DATE:  18-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P41 9439
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-546-4737
;      TELEFAX:  619-546-9392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1380 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  82..1329
;      OTHER INFORMATION:  /product= "HUMAN PITUITARY
;      OTHER INFORMATION:  CRF-RECEPTOR"
;      OTHER INFORMATION:  /note= "This sequence is encoded by clone
;      OTHER INFORMATION:  "CRF-R1"."
US-08-110-286A-1

  Query Match             4.9%;  Score 36;  DB 1;  Length 1380;
  Best Local Similarity   52.7%;  Pred. No. 0.18;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     188 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 247
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     862 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 921

Qy     248 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 307
            || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db     922 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 981

Qy     308 CACTCCAATGACCCCTACCACCAGTACA 335
           | |||          |   |||||||
Db     982 TCCACCACGTCTGAGACCATTCAGTACA 1009


RESULT 14
US-08-482-746-1
; Sequence 1, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
;  APPLICANT: Perrin, Marilyn H.
;  APPLICANT: Chen, Ruoping
;  APPLICANT: Lewis, Kathy A.
;  APPLICANT: Vale Jr., Wylie W.
;  APPLICANT: Donaldson, Cynthia J.
;  APPLICANT: Sawchenko, Paul
;  TITLE OF INVENTION: Cloning and Recombinant Production of
;  TITLE OF INVENTION: CRF Receptor(s)
;  FILE REFERENCE: P41-90002
;  CURRENT APPLICATION NUMBER: US/08/482,746B
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: US 08/374,009
;  EARLIER FILING DATE: 1995-01-17
;  EARLIER APPLICATION NUMBER: US 08/353,537
;  EARLIER FILING DATE: 1994-12-09
;  EARLIER APPLICATION NUMBER: PCT/US94/05908
;  EARLIER FILING DATE: 1994-05-25
;  EARLIER APPLICATION NUMBER: US 08/110,286
;  EARLIER FILING DATE: 1993-08-23
;  EARLIER APPLICATION NUMBER: US 08/079,320
;  EARLIER FILING DATE: 1993-06-18
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;  LENGTH: 1495
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (82)...(1326)
;  OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
;  OTHER INFORMATION: /note= "This sequence is encoded by clone
;  OTHER INFORMATION: "CRF-R1"."
US-08-482-746-1

  Query Match             4.9%;  Score 36;  DB 4;  Length 1495;
  Best Local Similarity   52.7%;  Pred. No. 0.19;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;
```

```
Qy     188 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 247
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     862 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 921

Qy     248 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 307
             ||  ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db     922 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 981

Qy     308 CACTCCAATGACCCCTACCACCAGTACA 335
             | |||          |   |||||||
Db     982 TCCACCACGTCTGAGACCATTCAGTACA 1009


RESULT 15
US-08-482-746-14
; Sequence 14, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
;  APPLICANT: Perrin, Marilyn H.
;  APPLICANT: Chen, Ruoping
;  APPLICANT: Lewis, Kathy A.
;  APPLICANT: Vale Jr., Wylie W.
;  APPLICANT: Donaldson, Cynthia J.
;  APPLICANT: Sawchenko, Paul
;  TITLE OF INVENTION: Cloning and Recombinant Production of
;  TITLE OF INVENTION: CRF Receptor(s)
;  FILE REFERENCE: P41-90002
;  CURRENT APPLICATION NUMBER: US/08/482,746B
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: US 08/374,009
;  EARLIER FILING DATE: 1995-01-17
;  EARLIER APPLICATION NUMBER: US 08/353,537
;  EARLIER FILING DATE: 1994-12-09
;  EARLIER APPLICATION NUMBER: PCT/US94/05908
;  EARLIER FILING DATE: 1994-05-25
;  EARLIER APPLICATION NUMBER: US 08/110,286
;  EARLIER FILING DATE: 1993-08-23
;  EARLIER APPLICATION NUMBER: US 08/079,320
;  EARLIER FILING DATE: 1993-06-18
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 1582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (82)...(1413)
;   OTHER INFORMATION: CRF-R splice-variant insert fragment inserted
;   OTHER INFORMATION: between  nucleotides 516-517 of SEQ ID NO:1.
;   OTHER INFORMATION: /note= "This sequence is contained in clone
;   OTHER INFORMATION: "CRF-R2"."
US-08-482-746-14

  Query Match             4.9%;  Score 36;  DB 4;  Length 1582;
  Best Local Similarity   52.7%;  Pred. No. 0.19;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     188 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 247
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     949 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 1008

Qy     248 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 307
             ||  ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db    1009 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 1068

Qy     308 CACTCCAATGACCCCTACCACCAGTACA 335
             | |||          |   |||||||
Db    1069 TCCACCACGTCTGAGACCATTCAGTACA 1096


Search completed: May 21, 2003, 21:39:31
Job time : 64.5504 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 19:16:44 ; Search time 178.18 Seconds
(without alignments)
9251.680 Million cell updates/sec

Title: US-09-550-163-1
Perfect score: 732
Sequence: 1 caaatccagaaaagatccgt.....atgaaaataaagccaaattt 732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	732	100.0	732	21	AAC64071	Human potassium ch
	2	732	100.0	732	24	AAD35170	Human KCNE2 wild t
	3	730.4	99.8	732	21	AAC64083	Human potassium ch
	4	730.4	99.8	732	21	AAC64084	Human potassium ch
	5	730.4	99.8	732	21	AAC64085	Human potassium ch
	6	730.4	99.8	732	21	AAC64086	Human potassium ch
	7	730.4	99.8	732	24	ABK86573	cDNA encoding huma
	8	730.4	99.8	732	24	AAD35169	Human KCNE2 mutant
	9	730.4	99.8	732	24	AAD35171	Human KCNE2 mutant
	10	730.4	99.8	732	24	AAD35172	Human KCNE2 mutant
	11	730.4	99.8	732	24	AAD35173	Human KCNE2 mutant
	12	553.8	75.7	600	22	ABA09192	Human MiRP1 homolo
	13	553.8	75.7	600	22	AAK52645	Human polynucleoti
	14	553.8	75.7	655	22	AAK51661	Human polynucleoti
	15	466	63.7	471	22	AAF80269	Nucleotide sequenc
	16	372	50.8	372	22	AAI24432	Probe #14365 for g
	17	372	50.8	372	22	AAI09965	Probe #9956 used t
	18	372	50.8	372	22	AAS00245	Human potassium ch
	19	368	50.3	450	22	ABA44797	Human breast cell
	20	368	50.3	450	22	ABA55252	Human foetal liver
	21	368	50.3	450	22	ABA24997	Probe #3463 for ge
	22	368	50.3	450	22	AAK03508	Human brain expres
	23	368	50.3	450	22	AAK28962	Human bone marrow
	24	368	50.3	450	22	AAI13549	Probe #3482 for ge
	25	368	50.3	450	22	AAI34911	Probe #3597 used t
	26	368	50.3	450	22	AAI03438	Probe #3429 used t
	27	368	50.3	450	24	ABS03496	Human genome-deriv
	28	312	42.6	312	22	ABA49938	Human breast cell
	29	312	42.6	312	22	ABA67856	Human foetal liver
	30	312	42.6	312	22	ABA34913	Probe #13379 for g
	31	312	42.6	312	22	AAK16264	Human brain expres
	32	312	42.6	312	22	AAK42008	Human bone marrow
	33	312	42.6	312	22	AAI22773	Probe #12706 for g
	34	312	42.6	312	22	AAI48075	Probe #16761 used
	35	312	42.6	312	22	AAI08446	Probe #8437 used t
	36	312	42.6	312	24	ABS16039	Human genome-deriv
	37	306	41.8	471	22	AAI15256	Probe #5189 for ge
	38	306	41.8	471	22	AAI04990	Probe #4981 used t
	39	277.4	37.9	468	21	AAC64072	Rat potassium chan
	40	266.4	36.4	372	22	AAS00246	Rat potassium chan
	41	60	8.2	60	24	ABN37461	Human spliced tran
	42	53.8	7.3	65	24	ABN29241	Rat spliced transc
c	43	53.2	7.3	231	22	ABA68478	Human foetal liver
c	44	53.2	7.3	231	22	ABA35463	Probe #13929 for g
c	45	53.2	7.3	231	22	AAK16847	Human brain expres

ALIGNMENTS

RESULT 1
AAC64071
ID AAC64071 standard; cDNA; 732 BP.
XX
AC AAC64071;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human potassium channel protein KCNE2 (MiRP1) cDNA, SEQ ID NO:1.
XX
KW Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW MinK-related; long QT syndrome; cardiac arrhythmia;
KW drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW HERG; ss.
XX
OS Homo sapiens.
XX
PN WO200063434-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10004.
XX
PR 15-APR-1999; 99US-0129404.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (UYYA) UNIV YALE.
XX
PI Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
XX
DR WPI; 2000-672747/65.

```
DR   P-PSDB; AAB29585.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 1; Page 118-119; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents cDNA encoding human KCNE2 (MiRP1).
XX
SQ   Sequence 732 BP; 221 A; 152 C; 157 G; 202 T; 0 other;

  Query Match             100.0%;  Score 732;  DB 21;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-203;
  Matches  732;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy     721 AAAGCCAAATTT 732
          ||||||||||||
Db     721 AAAGCCAAATTT 732


RESULT 2
AAD35170
ID   AAD35170 standard; DNA; 732 BP.
XX
AC   AAD35170;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human KCNE2 wild type DNA.
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "Human MiRP1 protein"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   P-PSDB; AAE22095.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 9; Page 43; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human KCNE2 wild type DNA.
XX
SQ   Sequence 732 BP; 221 A; 152 C; 157 G; 202 T; 0 other;

  Query Match             100.0%;  Score 732;  DB 24;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-203;
  Matches  732;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

```
RESULT 3
AAC64083
ID   AAC64083 standard; DNA; 732 BP.
XX
AC   AAC64083;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) Q9E mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29593.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 151 C; 158 G; 202 T; 0 other;
```

```
  Query Match             99.8%;  Score 730.4;  DB 21;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 9.2e-203;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACAGAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
```

```
Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

RESULT 4
AAC64084
ID AAC64084 standard; DNA; 732 BP.
XX
AC AAC64084;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human potassium channel protein KCNE2 (MiRP1) M54T mutant DNA.
XX
KW Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW MinK-related; long QT syndrome; cardiac arrhythmia;
KW drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW HERG; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200063434-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10004.
XX
PR 15-APR-1999; 99US-0129404.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (UYYA) UNIV YALE.
XX
PI Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
XX
DR WPI; 2000-672747/65.
DR P-PSDB; AAB29594.
XX
PT Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT diagnosing and treating ion channel disorders, especially long QT
PT syndrome -
XX
PS Claim 56; Page -; 132pp; English.

XX
CC The invention relates to novel ion channel proteins related to
CC KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC respectively). The cDNAs encoding these proteins are given in AAC64071-
CC AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC potassium channels (I-KR), mutations in which are associated with long
CC QT syndrome. The invention also relates to methods of diagnosing long QT
CC syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC nonhuman animals comprising a heterologous ion channel protein gene
CC of the invention, a transgenic animal comprising human KNCE2 and HERG
CC DNA, and methods of and screening drugs for treating long QT syndrome
CC using KCNE2 proteins (including mutants), nucleic acids encoding them
CC and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC acids, and proteins may be used for diagnosing or treating ion channel
CC disorders, especially long QT syndrome. Transgenic animals comprising
CC KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC The present sequence represents DNA encoding a mutant human KCNE2
CC (MiRP1) specifically claimed for use in diagnostic and drug screening
CC methods of the invention.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the wild-type human KNCE2 cDNA sequence shown on page
CC 118-119.
XX
SQ Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

Query Match 99.8%; Score 730.4; DB 21; Length 732;
Best Local Similarity 99.9%; Pred. No. 9.2e-203;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCACGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
```

```
Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy     721 AAAGCCAAATTT 732
           ||||||||||||
Db     721 AAAGCCAAATTT 732
```

RESULT 5
AAC64085
ID AAC64085 standard; DNA; 732 BP.
XX
AC AAC64085;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human potassium channel protein KCNE2 (MiRP1) I57T mutant DNA.
XX
KW Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW MinK-related; long QT syndrome; cardiac arrhythmia;
KW drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW HERG; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200063434-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10004.
XX
PR 15-APR-1999; 99US-0129404.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (UYYA) UNIV YALE.
XX
PI Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
XX
DR WPI; 2000-672747/65.
DR P-PSDB; AAB29595.
XX
PT Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT diagnosing and treating ion channel disorders, especially long QT
PT syndrome -
XX
PS Claim 56; Page -; 132pp; English.
XX
CC The invention relates to novel ion channel proteins related to
CC KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC respectively). The cDNAs encoding these proteins are given in AAC64071-
CC AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC potassium channels (I-KR), mutations in which are associated with long
CC QT syndrome. The invention also relates to methods of diagnosing long QT
CC syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC nonhuman animals comprising a heterologous ion channel protein gene
CC of the invention, a transgenic animal comprising human KNCE2 and HERG
CC DNA, and methods of and screening drugs for treating long QT syndrome
CC using KCNE2 proteins (including mutants), nucleic acids encoding them
CC and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC acids, and proteins may be used for diagnosing or treating ion channel
CC disorders, especially long QT syndrome. Transgenic animals comprising
CC KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC The present sequence represents DNA encoding a mutant human KCNE2
CC (MiRP1) specifically claimed for use in diagnostic and drug screening
CC methods of the invention.
CC Note: The present sequence is not shown in the specification, but is
CC derived from the wild-type human KNCE2 cDNA sequence shown on page
CC 118-119.
XX
SQ Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

Query Match 99.8%; Score 730.4; DB 21; Length 732;
Best Local Similarity 99.9%; Pred. No. 9.2e-203;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GACTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy     721 AAAGCCAAATTT 732
           ||||||||||||
Db     721 AAAGCCAAATTT 732
```

RESULT 6
AAC64086
ID AAC64086 standard; DNA; 732 BP.
XX
AC AAC64086;
XX
DT 19-FEB-2001 (first entry)

```
XX
DE   Human potassium channel protein KCNE2 (MiRP1) T8A mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29596.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 220 A; 152 C; 158 G; 202 T; 0 other;

  Query Match             99.8%;  Score 730.4;  DB 21;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 9.2e-203;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCGCACAGACGCTGGAAGACGTCTTCCG 120

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy     721 AAAGCCAAATTT 732
           ||||||||||||
Db     721 AAAGCCAAATTT 732


RESULT 7
ABK86573
ID   ABK86573 standard; DNA; 732 BP.
XX
AC   ABK86573;
XX
DT   24-SEP-2002  (first entry)
XX
DE   cDNA encoding human ether-a-go-go related interacting protein MiRP1.
XX
KW   Human; human ether-a-go-go related gene; HERG; KCR1; MiRP1;
KW   long QT syndrome; LQT; single nucleotide polymorphism; cardiac arrythmia;
KW   potassium channel; ss; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "MiRP1"
XX
PN   WO200242735-A2.
XX
PD   30-MAY-2002.
XX
PF   30-OCT-2001; 2001WO-US45644.
XX
```

```
PR   30-OCT-2000; 2000US-244340P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   Balser JR,  George AL,  Roden DM;
XX
DR   WPI; 2002-527650/56.
DR   P-PSDB; AAU99168.
XX
PT   Identifying a potassium channel activity modulator for drug design,
PT   comprises contacting a compound with a potassium channel and rat
PT   cerebellar cDNA library (KCR1) polypeptide, and determining activity -
XX
PS   Claim 17; Page 162-163; 164pp; English.
XX
CC   The invention relates to identifying (M1) a compound that modulates
CC   biological activity of a potassium channel (PC), by contacting a
CC   compound with a structure comprising a PC polypeptide and a polypeptide
CC   cloned from a rat cerebellar cDNA library (KCR1), and determining the
CC   activity of the PC polypeptide in the presence and absence of the
CC   compound, where a difference in the activities indicates modulation of
CC   biological activity of PC. Also include are identifying (M2) a candidate
CC   compound that modulates the biological activity of a complex comprising a
CC   human ether-a-go-go-related gene (HERG) channel polypeptide and a KCR1
CC   polypeptide, identifying (M3) a candidate compound as a modulator of KCR1
CC   expression, modulating (M4) PC function in a subject, comprising
CC   administering to the subject a substance that provides expression of a
CC   KCR1-encoding nucleic acid molecule in a cell or tissue, where modulated
CC   PC function is desired, screening (M5) for susceptibility to a drug-
CC   induced cardiac arrhythmia in a subject, comprising obtaining a
CC   biological sample from the subject and detecting a polymorphism of a KCR1
CC   gene in the biological sample from the subject, where the presence of the
CC   polymorphism indicates the susceptibility of the subject to a
CC   drug-induced cardiac arrhythmia, an oligonucleotide pair, where a first
CC   oligonucleotide of the pair hybridises to a first portion of a KCR1 gene
CC   which includes a polymorphism of the KCR1 gene, and the second
CC   oligonucleotide of the pair hybridises to a second portion of the KCR1
CC   gene that is adjacent to the first portion and a set of antisense
CC   oligonucleotide primers, suitable for amplifying a portion of a KCR1 gene
CC   which includes a polymorphism of the KCR1 gene. (M1) is useful for
CC   identifying a compound that modulates biological activity of PC,
CC   especially HERG, for modulating PC function (i.e modulating HERG
CC   activity) in a mammal, by preparing a composition comprising the
CC   compound and administering the composition. The compound is useful for
CC   treating or preventing long QT syndrome (LOT) and is useful in drug
CC   designing. The present sequence encodes a HERG interacting
CC   protein MiRP1 (not defined).
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

  Query Match             99.8%;  Score 730.4;  DB 24;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 9.2e-203;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy     721 AAAGCCAAATTT 732
           ||||||||||||
Db     721 AAAGCCAAATTT 732


RESULT 8
AAD35169
ID   AAD35169 standard; DNA; 732 BP.
XX
AC   AAD35169;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human KCNE2 mutant DNA (C420T).
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "Human MiRP1 mutant protein"
FT   variation       replace (420, C)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   P-PSDB; AAE22094.
XX
```

```
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 1; Page 41-42; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human KCNE2 mutant DNA (C420T).
XX
SQ   Sequence 732 BP; 221 A; 151 C; 157 G; 203 T; 0 other;

  Query Match             99.8%;  Score 730.4;  DB 24;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 9.2e-203;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGT 420

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy     721 AAAGCCAAATTT 732
           ||||||||||||
Db     721 AAAGCCAAATTT 732


RESULT 9
AAD35171
ID   AAD35171 standard; DNA; 732 BP.
XX
AC   AAD35171;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human KCNE2 mutant DNA (T234C).
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "Human MiRP1 mutant protein"
FT   variation       replace (234, T)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   P-PSDB; AAE22096.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 12; Page 44-45; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human KCNE2 mutant DNA (T234C).
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

  Query Match             99.8%;  Score 730.4;  DB 24;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 9.2e-203;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
```

```
Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCACGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

```
RESULT 10
AAD35172
ID   AAD35172 standard; DNA; 732 BP.
XX
AC   AAD35172;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human KCNE2 mutant DNA (T243C).
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "Human MiRP1 mutant protein"
FT   variation       replace (243, T)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   P-PSDB; AAE22097.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 15; Page 46; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human KCNE2 mutant DNA (T243C).
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
```

Query Match 99.8%; Score 730.4; DB 24; Length 732;
Best Local Similarity 99.9%; Pred. No. 9.2e-203;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
```

```
Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

RESULT 11
AAD35173
ID AAD35173 standard; DNA; 732 BP.
XX
AC AAD35173;
XX
DT 25-JUL-2002 (first entry)
XX
DE Human KCNE2 mutant DNA (A95G).
XX
KW Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
KW single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 74..445
FT /*tag= a
FT /product= "Human MiRP1 mutant protein"
FT variation replace (95, A)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN WO200222875-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-US28332.
XX
PR 11-SEP-2000; 2000US-231571P.
XX
PA (UYYA) UNIV YALE.
XX
PI Goldstein SAN;
XX
DR WPI; 2002-362360/39.
DR P-PSDB; AAE22098.
XX
PT Novel gene encoding Min-K related ion channel protein subunit and
PT polymorphisms in this gene associated with antibiotic-induced long QT
PT syndrome -
XX
PS Claim 18; Page 47-48; 49pp; English.
XX
CC The present invention relates to novel KCNE2 genes encoding Min-K related
CC (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC associated with ion channel disorders including antibiotic-induced long
CC QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC 57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC encoding the amino acid positions is useful for diagnosing the presence
CC of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC are useful in the development of new drug therapies which selectively
CC target one or more KCNE2 polymorphisms that are associated with cardiac
CC arrhythmias. The present sequence is human KCNE2 mutant DNA (A95G).
XX
SQ Sequence 732 BP; 220 A; 152 C; 158 G; 202 T; 0 other;

Query Match 99.8%; Score 730.4; DB 24; Length 732;

Best Local Similarity 99.9%; Pred. No. 9.2e-203;
Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCGCACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

RESULT 12
ABA09192
ID ABA09192 standard; cDNA; 600 BP.
XX
AC ABA09192;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human MiRP1 homologue-encoding cDNA, SEQ ID NO:968.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11948.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 826; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other;

Query Match 75.7%; Score 553.8; DB 22; Length 600;
Best Local Similarity 99.6%; Pred. No. 2.7e-151;

Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy     63 AGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAA 122
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 ATGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAA 86

Qy    123 GGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCC 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 GGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCC 146

Qy    183 TCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 TCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 206

Qy    243 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    207 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 266

Qy    303 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    267 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACA 326

Qy    363 AGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327 AGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGG 386

Qy    423 CTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCA 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    387 CTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCA 446

Qy    483 GACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 GACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGT 506

Qy    543 GAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATA 602
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    507 GAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATA 566

Qy    603 GATGACATTTCAATCTC 619
          |||||||||||||||||
Db    567 GATGACATTTCAATCTC 583
```

RESULT 13
AAK52645
ID AAK52645 standard; cDNA; 600 BP.
XX
AC AAK52645;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2174.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.

```
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79512.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 4539-4540; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other;

  Query Match            75.7%;  Score 553.8;  DB 22;  Length 600;
  Best Local Similarity  99.6%;  Pred. No. 2.7e-151;
  Matches  555;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      63 AGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAA 122
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27 ATGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAA 86

Qy     123 GGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCC 182
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      87 GGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCC 146

Qy     183 TCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     147 TCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 206

Qy     243 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     207 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 266

Qy     303 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACA 362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     267 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACA 326

Qy     363 AGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGG 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     327 AGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGG 386

Qy     423 CTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCA 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     387 CTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCA 446

Qy     483 GACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGT 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     447 GACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGT 506

Qy     543 GAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATA 602
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     507 GAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATA 566

Qy     603 GATGACATTTCAATCTC 619
           |||||||||||||||||
Db     567 GATGACATTTCAATCTC 583


RESULT 14
AAK51661
ID   AAK51661 standard; cDNA; 655 BP.
XX
AC   AAK51661;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 206.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM78528.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 1024; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 655 BP; 196 A; 154 C; 146 G; 153 T; 6 other;

  Query Match            75.7%;  Score 553.8;  DB 22;  Length 655;
  Best Local Similarity  99.6%;  Pred. No. 2.9e-151;
  Matches  555;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      63 AGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAA 122
```

```
Db     82 ATGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAA 141

Qy    123 GGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCC 182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 GGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCC 201

Qy    183 TCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 TCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 261

Qy    243 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 321

Qy    303 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACA 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACA 381

Qy    363 AGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 AGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGG 441

Qy    423 CTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCA 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 CTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTCCA 501

Qy    483 GACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGT 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 GACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAAGT 561

Qy    543 GAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATA 602
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    562 GAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGATA 621

Qy    603 GATGACATTTCAATCTC 619
          |||||||||||||||||
Db    622 GATGACATTTCAATCTC 638


RESULT 15
AAF80269
ID   AAF80269 standard; DNA; 471 BP.
XX
AC   AAF80269;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Nucleotide sequence of human potassium channel subunit IsK2.
XX
KW   Human; potassium channel; IsK2; gene therapy; gastric motility;
KW   gastric acid secretion; anti-arrhythmic agent; myocardial infarction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             79..450
FT                   /*tag= a
FT                   /product= "potassium channel subunit IsK2"
XX
PN   WO200127246-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-US28014.
XX
PR   12-OCT-1999;   99US-0158781.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Swanson RJ,  Liu Y,  Folander K;
XX
DR   WPI; 2001-273764/28.
DR   P-PSDB; AAB67800.
XX
PT   New DNA encoding the IsK2 potassium channel subunit, useful e.g. for
PT   detecting mutations and screening for therapeutic agents -
XX
PS   Claim 3; Fig 1A; 46pp; English.
XX
CC   The present sequence encodes a human potassium channel subunit,
CC   designated IsK2. The IsK2 polynucleotide, and derived probes, are
CC   used diagnostically to detect mutations in the IsK2 gene, to determine
CC   levels of mRNA expression and to isolate homologous sequences; for
CC   recombinant expression of IsK2; in gene therapy to increase potassium
CC   channel activity and to generate transgenic animals, as models and
CC   for drug screening. Recombinant IsK2 is used for studying biochemical
CC   activity of IsK2 and its role in disorders of gastric motility and
CC   gastric acid secretion, and to raise specific antibodies. IsK2
CC   modulators are potentially useful for treating diseases associated with
CC   increased or reduced potassium channel activity, e.g. as
CC   anti-arrhythmic agents for treating myocardial infarction and as
CC   regulators of gastric acid secretion.
XX
SQ   Sequence 471 BP; 143 A; 110 C; 103 G; 115 T; 0 other;

  Query Match          63.7%;  Score 466;  DB 22;  Length 471;
  Best Local Similarity  100.0%;  Pred. No. 1e-125;
  Matches  466;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 65

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 125

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    126 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 185

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 245

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 305

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 365

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 425

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGC 466
          |||||||||||||||||||||||||||||||||||||||||||||
Db    426 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGC 471


Search completed: May 21, 2003, 20:27:26
Job time : 183.18 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 19:44:14 ; Search time 1593.65 Seconds
(without alignments)
13367.622 Million cell updates/sec

Title: US-09-550-163-1
Perfect score: 732
Sequence: 1 caaatccagaaaagatccgt.....atgaaaataaagccaaattt 732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	732	100.0	732	6	AX406941	AX406941 Sequence
2	732	100.0	732	9	AF071002	AF071002 Homo sapi
3	730.4	99.8	732	6	AX406939	AX406939 Sequence
4	730.4	99.8	732	6	AX406943	AX406943 Sequence
5	730.4	99.8	732	6	AX406945	AX406945 Sequence
6	730.4	99.8	732	6	AX406947	AX406947 Sequence
7	730.4	99.8	24608	9	AP000320	AP000320 Homo sapi
8	730.4	99.8	100000	9	AP000052	AP000052 Homo sapi
9	730.4	99.8	100000	9	AP000167	AP000167 Homo sapi
10	730.4	99.8	100000	17	AP000120	Ap000120 Homo sapi
11	730.4	99.8	340000	9	AP001719	AP001719 Homo sapi
12	671	91.7	809	9	AF302095	AF302095 Homo sapi
13	292.2	39.9	1664	10	BC022699	BC022699 Mus muscu
14	277.4	37.9	468	10	AF071003	AF071003 Rattus no
c 15	273	37.3	144709	2	AC117904	AC117904 Rattus no
16	266.4	36.4	372	10	AY050513	AY050513 Cavia por
17	186.6	25.5	225	4	AY079211	AY079211 Sus scrof
18	186.2	25.4	215	4	AF329636	AF329636 Oryctolag
19	178.2	24.3	228	4	AF387764	AF387764 Equus cab
20	56	7.7	534	4	RABIPCS	L41659 Oryctolagus
21	55	7.5	750	10	GPIISK	L20462 Cavia cobay
22	53.2	7.3	390	9	AF135188	AF135188 Homo sapi
23	53.2	7.3	390	10	AY050512	AY050512 Cavia por
24	53.2	7.3	398	6	I40373	I40373 Sequence 5
25	53.2	7.3	402	9	HUMISKA	L33815 Homo sapien
26	53.2	7.3	408	9	HUMCDRPCA	L28168 Homo sapien
27	53.2	7.3	436	9	HUMISK	M26685 Human IsK p
28	53.2	7.3	1703	6	AR119312	AR119312 Sequence
29	53.2	7.3	1703	6	AR164693	AR164693 Sequence
30	53.2	7.3	3173	9	BC036452	BC036452 Homo sapi
c 31	53.2	7.3	43126	9	AP000324	AP000324 Homo sapi
c 32	53.2	7.3	100000	9	AP000053	AP000053 Homo sapi
c 33	53.2	7.3	100000	9	AP000168	AP000168 Homo sapi
c 34	53.2	7.3	100000	17	AP000121	Ap000121 Homo sapi
c 35	53.2	7.3	340000	9	AP001720	AP001720 Homo sapi
36	52.8	7.2	611	10	MMKCHA	X60457 M.musculus
37	52.6	7.2	393	4	AB032575	AB032575 Sus scrof
38	51	7.0	471	10	RATDRTKCA	M36461 Rat delayed
39	51	7.0	585	10	RATPCPA	M22412 Rat potassi
40	50.8	6.9	153306	2	AL807829	AL807829 Danio rer
41	50.4	6.9	390	4	MSU62404	U62404 Felis catus
42	44.6	6.1	422	12	SYNMINK	M64922 Synthetic v
43	43.2	5.9	209598	2	AC099473	AC099473 Rattus no
c 44	43.2	5.9	209598	2	AC099473	AC099473 Rattus no
c 45	42.4	5.8	122720	3	AC025721	AC025721 Caenorhab

ALIGNMENTS

RESULT 1
AX406941
LOCUS AX406941 732 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 3 from Patent WO0222875.
ACCESSION AX406941
VERSION AX406941.1 GI:21439816
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Goldstein,S.A.
TITLE Polymorphisms associated with cardiac arrythmia
JOURNAL Patent: WO 0222875-A 3 21-MAR-2002;

```
           YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, wild type"
                     /codon_start=1
                     /protein_id="CAD35180.1"
                     /db_xref="GI:21439817"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      221 a    152 c    157 g    202 t
ORIGIN

  Query Match           100.0%;  Score 732;  DB 6;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 4.6e-200;
  Matches  732;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

```
RESULT 2
AF071002
LOCUS       AF071002                732 bp    mRNA    linear   PRI 29-APR-1999
DEFINITION  Homo sapiens minK-related peptide 1 mRNA, complete cds.
ACCESSION   AF071002
VERSION     AF071002.1  GI:4704422
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   Abbott,G.W., Sesti,F., Splawski,I., Buck,M.E., Lehmann,M.H.,
            Timothy,K.W., Keating,M.T. and Goldstein,S.A.
  TITLE     MiRP1 forms IKr potassium channels with HERG and is associated with
            cardiac arrhythmia
  JOURNAL   Cell 97 (2), 175-187 (1999)
  MEDLINE   99235979
   PUBMED   10219239
REFERENCE   2  (bases 1 to 732)
  AUTHORS   Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Section of Developmental Biology and
            Biophysics, Department of Pediatrics and Boyer Center for Molecular
            Medicine, Yale University School of Medicine, 295 Congress Avenue,
            New Haven, CT 06536, USA
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q11.1"
                     /tissue_type="heart"
     CDS             74. .445
                     /note="potassium channel subunit; MiRP1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAD28086.1"
                     /db_xref="GI:4704423"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      221 a    152 c    157 g    202 t
ORIGIN

  Query Match           100.0%;  Score 732;  DB 9;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 4.6e-200;
  Matches  732;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
```

```
Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

```
RESULT 3
AX406939
LOCUS       AX406939                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 1 from Patent WO0222875.
ACCESSION   AX406939
VERSION     AX406939.1  GI:21439814
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 1 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Val substitued for Ala at
                     amino acid 116"
                     /codon_start=1
                     /protein_id="CAD35310.1"
                     /db_xref="GI:21439815"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGVAGFKMSP"
     variation       420
                     /note="The drug associated here was quinidine."
                     /replace="c"
BASE COUNT      221 a    151 c    157 g    203 t
ORIGIN
```

```
  Query Match             99.8%;  Score 730.4;  DB 6;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGT 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732
```

```
RESULT 4
AX406943
LOCUS       AX406943                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 5 from Patent WO0222875.
ACCESSION   AX406943
VERSION     AX406943.1  GI:21439818
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 5 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Thr substitued for Met at
                     amino acid 54"
                     /codon_start=1
                     /protein_id="CAD35181.1"
```

```
                     /db_xref="GI:21439819"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLTVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
     variation       234
                     /note="The drug associated here was procainamide."
                     /replace="t"
BASE COUNT      221 a    153 c    157 g    201 t
ORIGIN

  Query Match             99.8%;  Score 730.4;  DB 6;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCACGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732


RESULT 5
AX406945
LOCUS       AX406945                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 7 from Patent WO0222875.
ACCESSION   AX406945
VERSION     AX406945.1  GI:21439820
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 7 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Thr substituted for Ile at
                     amino acid 57"
                     /codon_start=1
                     /protein_id="CAD35311.1"
                     /db_xref="GI:21439821"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMTGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
     variation       243
                     /note="The drug associated here was oxatomide."
                     /replace="t"
BASE COUNT      221 a    153 c    157 g    201 t
ORIGIN

  Query Match             99.8%;  Score 730.4;  DB 6;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
```

```
Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732


RESULT 6
AX406947
LOCUS       AX406947                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 9 from Patent WO0222875.
ACCESSION   AX406947
VERSION     AX406947.1  GI:21439822
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 9 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Ala substitued for Thr at
                     amino acid 8"
                     /codon_start=1
                     /protein_id="CAD35312.1"
                     /db_xref="GI:21439823"
                     /translation="MSTLSNFAQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
     variation       95
                     /note="The drug associated here is was Bactrim."
                     /replace="a"
BASE COUNT      220 a    152 c    158 g    202 t
ORIGIN

  Query Match             99.8%;  Score 730.4;  DB 6;  Length 732;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCGCACAGACGCTGGAAGACGTCTTCCG 120

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db    721 AAAGCCAAATTT 732


RESULT 7
AP000320
LOCUS       AP000320               24608 bp    DNA     linear   PRI 20-NOV-1999
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
            clone:Q12C8, complete sequence.
ACCESSION   AP000320
VERSION     AP000320.1  GI:4835689
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:Q12C8.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24608)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Homo sapiens 24,608bp genomic DNA of 21q22.1
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 24608)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     The sequence is a part of the data (ACCESSION No. AP000165 -
            AP000173).
            The sequencing project is supported by Japan Science Technology
            Corporation (JST) and The Institute of Physical and Chemical
            Research (RIKEN).
FEATURES             Location/Qualifiers
     source          1. .24608
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
                     /clone="Q12C8"
BASE COUNT     6797 a   5420 c   5437 g   6954 t
ORIGIN
```

```
  Query Match             99.8%;  Score 730.4;  DB 9;  Length 24608;
  Best Local Similarity   99.9%;  Pred. No. 2.3e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15623 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 15682

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15683 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 15742

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15743 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 15802

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15803 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 15862

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15863 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 15922

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15923 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 15982

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15983 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 16042

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16043 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 16102

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16103 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 16162

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   16163 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 16222

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16223 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 16282

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16283 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 16342

Qy     721 AAAGCCAAATTT 732
          ||||||||||||
Db   16343 AAAGCCAAATTT 16354


RESULT 8
AP000052
LOCUS       AP000052              100000 bp    DNA     linear   PRI 20-NOV-1999
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28,
            complete sequence.
ACCESSION   AP000052
VERSION     AP000052.1  GI:3132362
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:245P17-f4A4f_2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA, chromosome 21q
  JOURNAL   Published Only in DataBase (1998)
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-1998) Masahira Hattori, Kitasato University,
            Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
            Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
            Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT     This sequence is conducted by Kitasato University JST sequencing
            Laboratory as a JST sequencing team.
            Principal Investigator:Yoshiyuki Sakaki Ph.D.
            Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
            sakaki@hgc.ims.u-tokyo.ac.jp
            Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
            sequence is submitted by:Human Genome Sequencing in ALIS project of
            JST
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0028 Japan
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top. html)
            or send email to webmaster@www-alis.tokyo.jst.go.jp'.
FEATURES             Location/Qualifiers
     source          1. .100000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
                     /clone="245P17-f4A4f_2"
BASE COUNT    27603 a  21934 c  22513 g  27950 t
ORIGIN

  Query Match             99.8%;  Score 730.4;  DB 9;  Length 100000;
  Best Local Similarity   99.9%;  Pred. No. 2.9e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80145 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 80204

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80205 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 80264

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80265 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 80324

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80325 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 80384

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80385 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 80444

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80445 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 80504

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80505 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 80564

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80565 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 80624

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80625 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 80684

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
```

```
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80685 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 80744

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80745 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 80804

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80805 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 80864

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db  80865 AAAGCCAAATTT 80876


RESULT 9
AP000167
LOCUS       AP000167               100000 bp    DNA     linear   PRI 08-JAN-2000
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
            clone B2344F14-f50E8, segment 3/9, complete sequence.
ACCESSION   AP000167
VERSION     AP000167.1  GI:4827132
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Homo sapiens 890,291bp genomic DNA of 21q22.1 (REGION: D21S226-AML
            CLONE RANGE: B2344F14-f50E8)
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     E. coli transposon insertion:The present data does not contain E.
            coli transposon sequences which integrated in the
            original/previous sequences.  We determined the boundary between
            the insertion and genomic sequences experimentally, removed the
            insertion sequences, reconstituted the present data. The sequencing
            project is supported by Japan Science Technology Corporation (JST)
            and The Institute of Physical and Chemical Research (RIKEN).
FEATURES             Location/Qualifiers
     source          1. .100000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
BASE COUNT    27338 a  22306 c  22571 g  27785 t
ORIGIN

  Query Match             99.8%;  Score 730.4;  DB 9;  Length 100000;
  Best Local Similarity   99.9%;  Pred. No. 2.9e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72113 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 72172

Qy     61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72173 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 72232

Qy    121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72233 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 72292

Qy    181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72293 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 72352

Qy    241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72353 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 72412

Qy    301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72413 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 72472

Qy    361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72473 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 72532

Qy    421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72533 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 72592

Qy    481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72593 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 72652

Qy    541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  72653 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 72712

Qy    601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72713 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 72772

Qy    661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72773 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 72832

Qy    721 AAAGCCAAATTT 732
          ||||||||||||
Db  72833 AAAGCCAAATTT 72844


RESULT 10
AP000120
ID   AP000120   standard; DNA; HUM; 100000 BP.
XX
AC   AP000120;
XX
SV   AP000120.1
XX
DT   04-MAY-1999 (Rel. 59, Created)
DT   26-SEP-1999 (Rel. 61, Last updated, Version 3)
XX
DE   Homo sapiens genomic DNA of 21q22.1, GART and AML related, SLC5A3-f4A4
DE   region, segment 3/8.
XX
KW   HTG.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-100000
RA   Hirakawa M., Yamaguchi H., Imai K., Shimada J.;
RT   ;
RL   Submitted (15-APR-1999) to the EMBL/GenBank/DDBJ databases.
RL   Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced
RL   Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan
RL   (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/,
RL   Tel:81-3-5214-8491, Fax:81-3-5214-8470)
```

```
XX
RN   [2]
RA   Hattori M., Ishii K., Toyoda A., Shiba T., Sakaki Y.;
RT   "Homo sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region";
RL   Unpublished.
XX
CC   This sequence is conducted by Kitasato University JST sequencing
CC   Laboratory as a JST sequencing team.
CC   Principal Investigator:Yoshiyuki Sakaki Ph.D.
CC   Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
CC   sakaki@hgc.ims.u-tokyo.ac.jp
CC   Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
CC   The sequence is submitted by Human Genome Sequencing in ALIS
CC   project of JST.
CC   Japan Science and Technology Corporation (JST)
CC   5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
CC   For further information about this sequence, including its
CC   location and relationship to other sequences, please visit our
CC   sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/)
CC   or send email to webmaster@www-alis.tokyo.jst.go.jp
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .100000
FT                   /chromosome="21"
FT                   /db_xref="taxon:9606"
FT                   /sequenced_mol="DNA"
FT                   /organism="Homo sapiens"
FT                   /map="21q22.1"
FT   STS             32213. .32320
FT                   /note="83F9aL-F/83F9aL-R;The location is between each
FT                   flanking site of PCR primers."
FT                   /standard_name="D21S1689"
FT   STS             43934. .44157
FT                   /note="AFMa086yf9;Genethon Marker;The location is between
FT                   each flanking site of PCR primers."
FT                   /standard_name="D21S1920"
XX
SQ   Sequence 100000 BP; 27731 A; 21990 C; 22220 G; 28059 T; 0 other;

  Query Match             99.8%;  Score 730.4;  DB 17;  Length 100000;
  Best Local Similarity   99.9%;  Pred. No. 2.9e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89447 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 89506

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89507 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 89566

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89567 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 89626

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89627 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 89686

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89687 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 89746

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89747 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 89806

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89807 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 89866

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89867 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 89926

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89927 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 89986

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   89987 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 90046

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90047 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 90106

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90107 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 90166

Qy     721 AAAGCCAAATTT 732
          ||||||||||||
Db   90167 AAAGCCAAATTT 90178


RESULT 11
AP001719
LOCUS       AP001719               340000 bp    DNA     linear   PRI 10-MAY-2000
DEFINITION  Homo sapiens genomic DNA, chromosome 21q, section 63/105.
ACCESSION   AP001719 AL163264 BA000005
VERSION     AP001719.1  GI:7768719
KEYWORDS    .
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
            Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
            Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
            Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
            Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
            Asakawa,S., Shintani,A., Sasaki,K., Nagamine,K., Mitsuyama,S.,
            Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
            Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
            Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
            Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
            Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
            Yaspo,M.L.
  TITLE     The DNA sequence of human chromosome 21
  JOURNAL   Nature 405 (6784), 311-319 (2000)
  MEDLINE   20289799
REFERENCE   2  (bases 1 to 340000)
  AUTHORS   Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
            Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
            Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
            Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
            Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
            Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
            Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
            Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
            Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
            Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
            Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
            Yaspo,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
            Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
            Group * Institute of Molecular Biotechnology, Genome Analysis *
            Keio University School of Medicine, Dept. of Molecular Biology *
            GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
            Genetics (addresses see below)
```

```
COMMENT     On May 30, 2000 this sequence version replaced gi:7717333.
            The chromosome 21 mapping and sequencing consortium consisting of
            * RIKEN Genomic Sciences Center, Human Genome Research Group, *
            Sagamihara 228-8555, Japan,
            * e.mail: hattori@gsc.riken.go.jp
            * URL: http://hgp.gsc.riken.go.jp/
            and
            * Institute of Molecular Biotechnology, Genome Analysis, *
            Beutenbergstrasse 11, D-07745 Jena, Germany,
            * e.mail: gscj-submit@genome.imb-jena.de
            * URL: http://genome.imb-jena.de/
            and
            * Keio University School of Medicine, Molecular Biology, * Tokyo
            160-8582, Japan,
            * e.mail: nshimizu@dmb-med.keio.ac.jp
            * URL: http://www.dmb.med.keio.ac.jp/
            and
            * GBF, Dept. of Genome Analysis,
            * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
            info.genome@gbf.de
            * URL: http://genome.gbf.de/
            and
            * Max-Planck Institute for Molecular Genetics,
            * Ihnestrasse 73, D-14195 Berlin, Germany,
            * e.mail: info-chr21@molgen.mpg.de
            * URL: http://chr21.rz-berlin.mpg.de/
            AL163264: Submitted (10-Apr-2000).
FEATURES              Location/Qualifiers
     source           1. .340000
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
     source           <1. .29420
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="R338L7, 5' partial"
                      /clone_lib="RPCI-11 BAC library"
                      /note="Accession No. AP000467"
     source           29242. .97350
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="CTD2344F14"
                      /clone_lib="CTD BAC library"
                      /note="Accession No. AP000315"
     source           96883. .121400
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="pS185"
                      /clone_lib="CMP21 P1 library"
                      /note="Accession No. AP000316"
     source           121210. .218631
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="P245P17"
                      /clone_lib="RP1 PAC library"
                      /note="Accession No. AP000317"
     source           218558. .260079
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="pQ6F8"
                      /clone_lib="CMP21 P1 library"
                      /note="Accession No. AP000318"
     source           258735. .285904
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="pQ94A10"
                      /clone_lib="CMP21 P1 library"
                      /note="Accession No. AP000319"
     source           285732. .310339
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="pQ12C8"
                      /clone_lib="CMP21 P1 library"
                      /note="Accession No. AP000320"
     source           310050. .326194
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="pQ82F5"
                      /clone_lib="CMP21 P1 library"
                      /note="Accession No. AP000321"
     source           325966. .>340000
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
                      /clone="pQ97G8, 3' partial"
                      /clone_lib="CMP21 P1 library"
                      /note="Accession No. AP000322"
     repeat_region    complement(1382. .1688)
                      /note="AluSp"
                      /rpt_family="SINE/Alu"
                      /rpt_type=DISPERSED
     repeat_region    complement(2099. .2390)
                      /note="AluSx"
                      /rpt_family="SINE/Alu"
                      /rpt_type=DISPERSED
     repeat_region    2799. .2884
                      /note="MIR"
                      /rpt_family="SINE/MIR"
                      /rpt_type=DISPERSED
     repeat_region    complement(2891. .3287)
                      /note="MER31A"
                      /rpt_family="LTR/MER4-group"
                      /rpt_type=DISPERSED
     repeat_region    3288. .3381
                      /note="MIR"
                      /rpt_family="SINE/MIR"
                      /rpt_type=DISPERSED
     misc_feature     4211. .5231
                      /note="CpG island"
     misc_feature     4272. .4279
                      /note="NotI site"
     repeat_region    4328. .4476
                      /note="(CGGGG)n"
                      /rpt_family="Simple_repeat"
                      /rpt_type=TANDEM
     gene             4392. .35127
                      /gene="SLC5A3"
     mRNA             join(4392. .4740,12254. .35127)
                      /gene="SLC5A3"
                      /product="Sodium/myo-inositol cotransporter"
                      /note="human solute carrier family 5, member 3, Accession
                      No. AF027153"
     exon             4392. .4740
                      /gene="SLC5A3"
                      /number=1
     misc_feature     4392. .4399
                      /gene="SLC5A3"
                      /note="NotI site"
     repeat_region    4810. .4985
```

```
                     /note="(CGGG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM
     repeat_region   5099. .5191
                     /note="(CCG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM

  Query Match             99.8%;  Score 730.4;  DB 9;  Length 340000;
  Best Local Similarity   99.9%;  Pred. No. 3.4e-199;
  Matches  731;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301354 CAAATCCAGAAAAGATCCGTTTTCCTAACCTTGTTCGCCTATTTTATTATTTAAATTGCA 301413

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301414 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 301473

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301474 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 301533

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301534 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 301593

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301594 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 301653

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301654 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 301713

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301714 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 301773

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301774 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 301833

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301834 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 301893

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  301894 GTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 301953

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301954 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 302013

Qy     661 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  302014 AGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAAT 302073

Qy     721 AAAGCCAAATTT 732
          ||||||||||||
Db  302074 AAAGCCAAATTT 302085


RESULT 12
AF302095
LOCUS       AF302095                809 bp    mRNA    linear   PRI 14-SEP-2000
DEFINITION  Homo sapiens voltage-gated K+ channel subunit MIRP1 (KCNE2) mRNA,
            complete cds.
ACCESSION   AF302095
VERSION     AF302095.1  GI:10121887
KEYWORDS    .

SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 809)
  AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
  TITLE     Cloning of human MIRP1 cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 809)
  AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2000) Medical and Molecular Genetics Center,
            Institut Recerca Oncologica, Avia. de Castelldefels Km 2,7,
            L'Hospitalet de Llobregat, Barcelona 08907, Spain
FEATURES             Location/Qualifiers
     source          1. .809
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22"
     gene            1. .809
                     /gene="KCNE2"
     CDS             141. .512
                     /gene="KCNE2"
                     /codon_start=1
                     /product="voltage-gated K+ channel subunit MIRP1"
                     /protein_id="AAG13416.1"
                     /db_xref="GI:10121888"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      247 a    172 c    189 g    200 t      1 others
ORIGIN

  Query Match             91.7%;  Score 671;  DB 9;  Length 809;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-182;
  Matches  671;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      60 AGCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCC 119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 AGCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCC 186

Qy     120 GAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGG 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 GAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGG 246

Qy     180 CCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGA 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 CCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGA 306

Qy     240 TGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGA 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 TGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGA 366

Qy     300 GACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGT 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 GACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGT 426

Qy     360 ACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 ACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTG 486

Qy     420 CGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 CGGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGT 546

Qy     480 CCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAA 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 CCAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAA 606

Qy     540 AGTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAG 599
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     607 AGTGAGTTCCTTGCTCTCTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAG 666
```

```
Qy    600 ATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTG 659
          ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db    667 ATAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGKTGGAGCAATATTTTGTGCTG 726

Qy    660 AAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAA 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 AAGACCTCTTTTACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGAAAA 786

Qy    720 TAAAGCCAAATTT 732
          |||||||||||||
Db    787 TAAAGCCAAATTT 799
```

```
RESULT 13
BC022699
LOCUS       BC022699               1664 bp    mRNA    linear   ROD 07-AUG-2002
DEFINITION  Mus musculus, RIKEN cDNA 2200002I16 gene, clone MGC:31447
            IMAGE:4481325, mRNA, complete cds.
ACCESSION   BC022699
VERSION     BC022699.1  GI:18490550
KEYWORDS    MGC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1664)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 44 Row: a Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES             Location/Qualifiers
     source          1. .1664
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="MGC:31447 IMAGE:4481325"
                     /tissue_type="Eye, retina, mouse strain C57Bl\6"
                     /clone_lib="NIH_MGC_94"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             90. .461
                     /codon_start=1
                     /product="RIKEN cDNA 2200002I16 gene"
                     /protein_id="AAH22699.1"
                     /db_xref="GI:18490551"
                     /db_xref="LocusID:69143"
                     /translation="MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAE
                     NFYYVILYLMVMIGMFSFIVVAILVSTVKSKRREHSQHPYHQYIVEDWQEKYKSQILH
                     LEDSKATIHENMGATGFTVSP"
BASE COUNT      502 a    337 c    404 g    421 t
ORIGIN
```

```
  Query Match           39.9%;  Score 292.2;  DB 10;  Length 1664;
  Best Local Similarity   68.9%;  Pred. No. 4.6e-73;
  Matches  464;  Conservative    0;  Mismatches  168;  Indels   41;  Gaps    3;

Qy      61 GCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG 120
           ||| | |||||||||| | || ||| ||||||| || ||||| ||||| || | ||||
Db      77 GCAAGGGGGAAGCATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAA 136

Qy     121 AAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGC 180
           || ||||||||||||||||||||||  ||| |   |||||| ||||| ||| |  ||||
Db     137 AAAGATTTTTATTACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGC 196

Qy     181 CCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGAT 240
           ||||| |||| ||| ||||| ||||||||||||| ||||||||||||||||||||||||
Db     197 ACTCCAGGCCAGAGTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGAT 256

Qy     241 GATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAG 300
           ||| || |||||||| |||||| | ||||||||||||||||||| ||||| || ||| |
Db     257 GATCGGCATGTTCTCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCG 316

Qy     301 ACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTA 360
           || || |||||| |  |||| ||||||||||||| || || || ||||||||||||||
Db     317 GCGAGAGCACTCCCAGCACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTA 376

Qy     361 CAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGC 420
           ||| || || ||| || |||| ||||| || |||||||||||||||||||||||| || ||
Db     377 CAAAAGTCAGATCCTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACATGGGGGC 436

Qy     421 GGCTGGGTTCAAAATGTCCCCCTGATAAGGGAGAAAGGCACCAAGCTAACATCTGACGTC 480
           | | ||||||| | |||| |||||||     || || |                ||||
Db     437 GACGGGGTTCACAGTGTCACCCTGATTGATAAGGAATGGGGGCC------------CGTC 484

Qy     481 CAGACATGAAGAGATGCCAGTGCCACGAGGCAAATCCAAATTGTCTTTGCTTAGAAGAAA 540
             |    ||   | |||   |||  |   |  |  || | ||||  ||||| |||||| |
Db     485 TGGCTCAGACAGGGTGCTTCTGCTGCCTCGAGAGCCCCACTTGTGCTTGCTCAGAAGACA 544

Qy     541 GTGAGTTCCTTGCTCTTTGTTGAGAATTTTCATGGAGATTATGTGGTTGGCCAATAAAGA 600
           |  |||||||   |      ||             | |
Db     545 GCTAGTTCCTCTGTGCAGCCTGGCTGGCAGTTGACACAG---------------------- 583

Qy     601 TAGATGACATTTCAATCTCAGTGATTTATGCTTGCTTGTTGGAGCAATATTTTGTGCTGA 660
               ||||||||| ||||||||| |||| |   || |||||| |  ||| ||| |||| |
Db     584 ----TGACATTTCTATCTCAGTGGTTTAGGTGAGCCTGTTGGGGTGATACTTTATGCTAA 639

Qy     661 AGACCTCTTTT----ACTTTCCGGGCAAGTGAATGTCATTTTAATCAATATCAATGATGA 716
           || |||||||      | |   |  | || | ||| ||||||| |||| ||||| ||||
Db     640 GGATCTCTTTTTTCACATGTTATGCAATGTAACTGTTATTTTAAACAATTTCAATCATGA 699

Qy     717 AAATAAAGCCAAA 729
           || | || ||||
Db     700 GAACAGAGGCAAA 712
```

```
RESULT 14
AF071003
LOCUS       AF071003               468 bp    mRNA    linear   ROD 29-APR-1999
DEFINITION  Rattus norvegicus minK-related peptide 1 mRNA, complete cds.
ACCESSION   AF071003
VERSION     AF071003.1  GI:4704424
KEYWORDS    .
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Abbott,G.W., Sesti,F., Splawski,I., Buck,M.E., Lehmann,M.H.,
            Timothy,K.W., Keating,M.T. and Goldstein,S.A.
  TITLE     MiRP1 forms IKr potassium channels with HERG and is associated with
            cardiac arrhythmia
  JOURNAL   Cell 97 (2), 175-187 (1999)
  MEDLINE   99235979
   PUBMED   10219239
```

```
REFERENCE   2  (bases 1 to 468)
  AUTHORS   Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Section of Developmental Biology and
            Biophysics, Department of Pediatrics and Boyer Center for Molecular
            Medicine, Yale University School of Medicine, 295 Congress Avenue,
            New Haven, CT 06536, USA
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /sex="male"
                     /tissue_type="heart"
                     /dev_stage="10-12 weeks"
     CDS             35. .406
                     /note="potassium channel subunit; MiRP1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAD28087.1"
                     /db_xref="GI:4704425"
                     /translation="MTTLANLTQTLEDAFKKVFITYMDSWRRNTTAEQQALQARVDAE
                     NFYYVILYLMVMIGMFAFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILH
                     LEDSKATIHENLGATGFTVSP"
BASE COUNT      118 a    126 c    131 g     93 t
ORIGIN

  Query Match             37.9%;  Score 277.4;  DB 10;  Length 468;
  Best Local Similarity   81.8%;  Pred. No. 7e-69;
  Matches  320;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy      62 CAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGA 121
           || | ||||| |||| | |||||| |||| || || ||||| ||||| || | ||||  |
Db      23 CAAGGGGGAAACATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAA 82

Qy     122 AGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCC 181
           | | |||| ||||||||||||||||  ||| |   |||||||||||| || ||| ||||
Db      83 AAGGTTTTCATTACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCG 142

Qy     182 CTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATG 241
           ||||| |||| ||| ||||| ||||||||||||||| ||||||||||||||||||||||||
Db     143 CTCCAGGCCAGAGTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATG 202

Qy     242 ATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGA 301
           || || |||||| | |||||| | ||||||||||||||||||| ||||| || ||| |
Db     203 ATCGGCATGTTCGCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGG 262

Qy     302 CGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTAC 361
           ||||| |||||| | |||| ||||||||||||| || ||||| |||||| | |||||
Db     263 CGGGAGCACTCCCAGGACCCGTACCACCAGTACATCGTGGAGGATTGGCAGCAGAAGTAT 322

Qy     362 AAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCG 421
           | ||| || |||||| |||| ||||| || |||||||||||||||||||| | || |||
Db     323 AGGAGTCAGATCTTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACCTGGGGGCG 382

Qy     422 GCTGGGTTCAAAATGTCCCCCTGATAAGGGA 452
           | ||||||| | |||| |||||||||| | |
Db     383 ACGGGGTTCACAGTGTCACCCTGATAAAGAA 413


RESULT 15
AC117904/c
LOCUS       AC117904              144709 bp    DNA     linear   HTG 18-JUL-2002
DEFINITION  Rattus norvegicus clone CH230-409A1, *** SEQUENCING IN PROGRESS
            ***, 44 unordered pieces.
ACCESSION   AC117904
VERSION     AC117904.3  GI:21746840
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 144709)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
            Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
            Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
            Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
            Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
            Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
            Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
            Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 144709)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-APR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 144709)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jul 14, 2002 this sequence version replaced gi:20162905.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GVCH
                Center clone name: CH230-409A1
            -------------- Summary Statistics
                Sequencing vector: Plasmid;
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 112047 bases at least Q40
                Consensus quality: 117676 bases at least Q30
                Consensus quality: 121024 bases at least Q20
            --------------
            * NOTE: Estimated insert size may differ from sequence length
```

```
*   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*        1     1015: contig of 1015 bp in length
*     1016     1115: gap of unknown length
*     1116     2338: contig of 1223 bp in length
*     2339     2438: gap of unknown length
*     2439     3686: contig of 1248 bp in length
*     3687     3786: gap of unknown length
*     3787     5609: contig of 1823 bp in length
*     5610     5709: gap of unknown length
*     5710     7138: contig of 1429 bp in length
*     7139     7238: gap of unknown length
*     7239     9288: contig of 2050 bp in length
*     9289     9388: gap of unknown length
*     9389    11561: contig of 2173 bp in length
*    11562    11661: gap of unknown length
*    11662    12758: contig of 1097 bp in length
*    12759    12858: gap of unknown length
*    12859    15068: contig of 2210 bp in length
*    15069    15168: gap of unknown length
*    15169    16496: contig of 1328 bp in length
*    16497    16596: gap of unknown length
*    16597    19364: contig of 2768 bp in length
*    19365    19464: gap of unknown length
*    19465    20896: contig of 1432 bp in length
*    20897    20996: gap of unknown length
*    20997    22441: contig of 1445 bp in length
*    22442    22541: gap of unknown length
*    22542    24534: contig of 1993 bp in length
*    24535    24634: gap of unknown length
*    24635    27140: contig of 2506 bp in length
*    27141    27240: gap of unknown length
*    27241    29139: contig of 1899 bp in length
*    29140    29239: gap of unknown length
*    29240    31805: contig of 2566 bp in length
*    31806    31905: gap of unknown length
*    31906    34154: contig of 2249 bp in length
*    34155    34254: gap of unknown length
*    34255    36644: contig of 2390 bp in length
*    36645    36744: gap of unknown length
*    36745    37831: contig of 1087 bp in length
*    37832    37931: gap of unknown length
*    37932    39841: contig of 1910 bp in length
*    39842    39941: gap of unknown length
*    39942    42387: contig of 2446 bp in length
*    42388    42487: gap of unknown length
*    42488    45137: contig of 2650 bp in length
*    45138    45237: gap of unknown length
*    45238    48966: contig of 3729 bp in length
*    48967    49066: gap of unknown length
*    49067    51971: contig of 2905 bp in length
*    51972    52071: gap of unknown length
*    52072    54562: contig of 2491 bp in length
*    54563    54662: gap of unknown length
*    54663    56481: contig of 1819 bp in length
*    56482    56581: gap of unknown length
*    56582    59476: contig of 2895 bp in length
*    59477    59576: gap of unknown length
*    59577    63124: contig of 3548 bp in length
*    63125    63224: gap of unknown length
*    63225    67624: contig of 4400 bp in length
*    67625    67724: gap of unknown length
*    67725    71583: contig of 3859 bp in length
*    71584    71683: gap of unknown length
*    71684    75653: contig of 3970 bp in length
*    75654    75753: gap of unknown length
*    75754    79243: contig of 3490 bp in length
*    79244    79343: gap of unknown length
*    79344    82996: contig of 3653 bp in length
*    82997    83096: gap of unknown length
*    83097    88441: contig of 5345 bp in length
*    88442    88541: gap of unknown length
*    88542    92876: contig of 4335 bp in length
*    92877    92976: gap of unknown length
*    92977    97178: contig of 4202 bp in length
*    97179    97278: gap of unknown length
*    97279   103933: contig of 6655 bp in length
*   103934   104033: gap of unknown length
*   104034   109263: contig of 5230 bp in length
*   109264   109363: gap of unknown length
*   109364   115319: contig of 5956 bp in length
*   115320   115419: gap of unknown length
*   115420   122481: contig of 7062 bp in length
*   122482   122581: gap of unknown length
*   122582   132083: contig of 9502 bp in length
*   132084   132183: gap of unknown length
*   132184   139601: contig of 7418 bp in length
*   139602   139701: gap of unknown length
*   139702   144709: contig of 5008 bp in length.
FEATURES             Location/Qualifiers
     source          1. .144709
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /clone="CH230-409A1"
BASE COUNT    36065 a  34426 c  33378 g  36487 t   4353 others
ORIGIN

  Query Match             37.3%;  Score 273;  DB 2;  Length 144709;
  Best Local Similarity   81.2%;  Pred. No. 3.2e-67;
  Matches  329;  Conservative    0;  Mismatches   75;  Indels    1;  Gaps    1;

Qy      59 CAGCAGGAGGGAAGCATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTC 118
           ||||| | ||||| |||| | |||||| |||| || || ||||| ||||| || | ||||
Db 131731 CAGCAAGGGGGAAACATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTC 131672

Qy     119 CGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAG 178
             || | |||| |||||||||||||||  ||| |   |||||||||||| || ||| ||
Db 131671 AAAAAGGTTTTCATTACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAG 131612

Qy     179 GCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTG 238
           || ||||| |||| ||| |||||| ||||||||||||||| ||||||||||||||||||||
Db 131611 GCGCTCCAGGCCAGAGTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTG 131552

Qy     239 ATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAG 298
           ||||| || |||||| | |||||| | ||||||||||||||||||||| ||||| || |||
Db 131551 ATGATCGGCATGTTCGCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAG 131492

Qy     299 AGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAG 358
            | ||||| |||||| | ||||| |||||||||||||| || ||||| |||||| | |||
Db 131491 CGGCGGGAGCACTCCCAGGACCCGTACCACCAGTACATCGTGGAGGATTGGCAGCAGAAG 131432

Qy     359 TACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGT 418
           || | ||| || |||||| |||| ||||| || |||| |||||||||||||||| | ||
Db 131431 TATAGGAGTCAGATCTTGCATCTGGAAGACTCCAAGGGCACCATCCATGAGAACCTGGGG 131372

Qy     419 GCGGCTGGGTTCAAAATGTC-CCCCTGATAAGGGAGAAAGGCACC 462
           ||| | ||||||| | |||| ||||||||||   || || || |
Db 131371 GCGACCGGGTTCACAGTGTCACCCCTGATAAGAACGAGAGTCATC 131327


Search completed: May 21, 2003, 21:16:17
Job time : 2113.65 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 14:15:58 ; Search time 13 Seconds
(without alignments)
392.430 Million cell updates/sec

Title: US-09-550-163-2
Perfect score: 632
Sequence: 1 MSTLSNFTQTLEDVFRRIFI.....EESKATIHENIGAAGFKMSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	632	100.0	123	1	MIR1_HUMAN	Q9y6j6 homo sapien
2	554	87.7	123	1	MIR1_RAT	Q9wtw0 rattus norv
3	132.5	21.0	129	1	MINK_HUMAN	P15382 homo sapien
4	130.5	20.6	129	1	MINK_FELCA	Q9xspl felis silve
5	128.5	20.3	129	1	MINK_MOUSE	P23299 mus musculu
6	128	20.3	130	1	MINK_RAT	P15383 rattus norv
7	127.5	20.2	130	1	MINK_PIG	Q9tuh9 sus scrofa
8	126.5	20.0	125	1	MINK_CAVPO	Q60409 cavia porce
9	125	19.8	130	1	MINK_RABIT	Q28705 oryctolagus
10	84.5	13.4	439	1	YZ04_METJA	Q60260 methanococc
11	76.5	12.1	557	1	CPS_CLOTM	Q02929 clostridium
12	76	12.0	103	1	MIR2_HUMAN	Q9y6h6 homo sapien
13	74.5	11.8	1042	1	SYI_BORBU	O51773 borrelia bu
14	74	11.7	938	1	V120_HSV7J	P52438 human herpe
15	73.5	11.6	497	1	NU2M_CHOCR	P48903 chondrus cr
16	73	11.6	400	1	TYRP_HAEIN	P44727 haemophilus
17	72	11.4	103	1	MIR2_MOUSE	Q9wtw2 mus musculu
18	71.5	11.3	107	1	MIR2_RAT	Q9jjv7 rattus norv
19	71	11.2	291	1	ATHB_RABIT	P18597 oryctolagus
20	70.5	11.2	874	1	SYV_UREPA	Q9pqm4 ureaplasma
21	70	11.1	170	1	MIR3_MOUSE	Q9wtw3 mus musculu
22	69.5	11.0	946	1	YBT6_YEAST	P38250 saccharomyc
23	68.5	10.8	701	1	TP20_YEAST	P33891 saccharomyc
24	68.5	10.8	1007	1	RGA1_YEAST	P39083 saccharomyc
25	68	10.8	518	1	HEMK_RICPR	Q9zcb3 rickettsia
26	68	10.8	774	1	YMA6_YEAST	Q04233 saccharomyc
27	68	10.8	1175	1	SRS2_YEAST	P12954 saccharomyc
28	68	10.8	1607	1	MIPR_LYMST	Q25410 lymnaea sta
29	67.5	10.7	453	1	YWZ5_CAEEL	Q11095 caenorhabdi
30	67.5	10.7	1972	1	MYHB_RABIT	P35748 oryctolagus
31	67	10.6	476	1	YG12_YEAST	P53201 saccharomyc
32	66.5	10.5	752	1	PA26_MOUSE	P97819 mus musculu
33	66.5	10.5	1197	1	DPOM_PODAN	Q01529 podospora a
34	66	10.4	210	1	MT04_MYCGE	P47589 mycoplasma
35	66	10.4	2146	1	INSR_DROME	P09208 drosophila
36	65.5	10.4	987	1	EPB4_HUMAN	P54760 homo sapien
37	65.5	10.4	987	1	EPB4_MOUSE	P54761 mus musculu
38	65.5	10.4	2016	1	CIN5_HUMAN	Q14524 homo sapien
39	65.5	10.4	2019	1	CIN5_RAT	P15389 rattus norv
40	65	10.3	471	1	YL57_CAEEL	P34437 caenorhabdi
41	65	10.3	622	1	ME25_SCHPO	Q9p6s4 schizosacch
42	65	10.3	629	1	SYM_THEMA	O33925 thermotoga
43	65	10.3	1835	1	CCAI_RAT	Q9z0y8 rattus norv
44	64.5	10.2	556	1	YMC3_YEAST	Q03718 saccharomyc
45	64.5	10.2	809	1	PLSB_PASMU	Q9cln7 pasteurella

ALIGNMENTS

RESULT 1
MIR1_HUMAN
ID MIR1_HUMAN STANDARD; PRT; 123 AA.
AC Q9Y6J6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Minimum potassium ion channel-related peptide 1 (MiRP1) (MinK-related
DE peptide 1).
GN KCNE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., VARIANTS LQT6 E-9; T-54 AND T-57, AND VARIANT A-8.
RC TISSUE=Heart;
RX MEDLINE=99235979; PubMed=10219239;
RA Abbott G.W., Sesti F., Splawski I., Buck M.E., Lehmann M.H.,
RA Timothy K.W., Keating M.T., Goldstein S.A.N.;
RT "MiRP1 forms IKr potassium channels with HERG and is associated with
RT cardiac arrhythmia.";
RL Cell 97:175-187(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Domenech A., Estivill X., de la Luna S.;
RT "Cloning of human MIRP1 cDNA.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP ASSOCIATION WITH KCNQ2/KCNQ3, AND TISSUE SPECIFICITY.
RX MEDLINE=20487128; PubMed=11034315;
RA Tinel N., Diochot S., Lauritzen I., Barhanin J., Lazdunski M.,
RA Borsotto M.;
RT "M-type KCNQ2-KCNQ3 potassium channels are modulated by the KCNE2
RT subunit.";
RL FEBS Lett. 480:137-141(2000).
CC -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC STABILITY OF THE MULTIMERIC COMPLEX. KCNE2 CO-ASSEMBLE WITH KCNH2
CC (HERG) TO FORM THE CARDIAC POTASSIUM (IKR) CHANNEL. MAY ALSO
CC ASSOCIATE WITH KCNQ2 AND/OR KCNQ3 TO FORM A POTASSIUM CHANNEL WITH
CC ESSENTIALLY IDENTICAL PROPERTIES TO THE CHANNEL UNDERLYING THE
CC NATIVE M-CURRENT, A SLOWLY ACTIVATING AND DEACTIVATING POTASSIUM
CC CONDUCTANCE WHICH PLAYS A CRITICAL ROLE IN DETERMINING THE
CC SUBTHRESHOLD ELECTRICAL EXCITABILITY OF NEURONS. MAY ACT AS A
CC REGULATORY SUBUNIT OF THE KCNQ2/KCNQ3 M-TYPE CHANNEL.
CC -!- SUBUNIT: ASSOCIATES WITH KCNH2. MAY ASSOCIATE WITH KCNQ2 AND/OR
CC KCNQ3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, HEART, SKELETAL
CC MUSCLE, PANCREAS, PLACENTA, KIDNEY, COLON AND THYMUS. A SMALL BUT
CC SIGNIFICANT EXPRESSION IS FOUND IN LIVER, OVARY, TESTIS, PROSTATE,
CC SMALL INTESTINE AND LEUKOCYTES. VERY LOW EXPRESSION, NEARLY
CC UNDETECTABLE, IN LUNG AND SPLEEN.
CC -!- DISEASE: DEFECTS IN KCNE2 ARE THE CAUSE OF LONG QT SYNDROME TYPE 6
CC (LQT6); A FORM OF HEART DISEASE CHARACTERIZED BY CARDIAC

```
CC       ARRHYTHMIA. MUTANTS FORM CHANNELS THAT OPEN SLOWLY AND CLOSE
CC       RAPIDLY, THEREBY DIMINISHING POTASSIUM CURRENTS.
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   -!- DATABASE: NAME=LQTSdb; NOTE=KCNE2 mutations page;
CC       WWW="http://Www.ssi.dk/en/forskning/lqtsdb/kcne2.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF071002; AAD28086.1; -.
DR   EMBL; AF302095; AAG13416.1; -.
DR   Genew; HGNC:6242; KCNE2.
DR   MIM; 603796; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation; Disease mutation; Polymorphism;
KW   Long QT syndrome.
FT   DOMAIN       1     48       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     49    69       POTENTIAL.
FT   DOMAIN       70    123      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     6     6        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     29    29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES      71    71       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES      74    74       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   VARIANT      8     8        T -> A.
FT                               /FTId=VAR_008375.
FT   VARIANT      9     9        Q -> E (IN LQT6; IMPEDES ACTIVATION AND
FT                               INCREASES SENSITIVITY TO MACROLIDE
FT                               ANTIBIOTICS).
FT                               /FTId=VAR_008376.
FT   VARIANT      54    54       M -> T (IN LQT6; FORMS I(KR) CHANNELS
FT                               THAT DEACTIVATE TWICE AS FAST AS WILD
FT                               TYPE).
FT                               /FTId=VAR_008377.
FT   VARIANT      57    57       I -> T (IN LQT6).
FT                               /FTId=VAR_008378.
SQ   SEQUENCE   123 AA;  14471 MW;  C3016415E1B44890 CRC64;

  Query Match             100.0%;  Score 632;  DB 1;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-56;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 2
MIR1_RAT
ID   MIR1_RAT       STANDARD;      PRT;   123 AA.
AC   Q9WTW0;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Minimum potassium ion channel-related peptide 1 (MiRP1) (MinK-related
DE   peptide 1).
GN   KCNE2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Heart;
RX   MEDLINE=99235979; PubMed=10219239;
RA   Abbott G.W., Sesti F., Splawski I., Buck M.E., Lehmann M.H.,
RA   Timothy K.W., Keating M.T., Goldstein S.A.N.;
RT   "MiRP1 forms IKr potassium channels with HERG and is associated with
RT   cardiac arrhythmia.";
RL   Cell 97:175-187(1999).
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE2 CO-ASSEMBLE WITH KCNH2
CC       (HERG) TO FORM THE CARDIAC POTASSIUM (IKR) CHANNEL.
CC   -!- SUBUNIT: ASSOCIATES WITH KCNH2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF071003; AAD28087.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN       1     48       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     49    69       POTENTIAL.
FT   DOMAIN       70    123      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     6     6        N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     29    29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES      71    71       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES      74    74       PHOSPHORYLATION (BY PKC) (POTENTIAL).
SQ   SEQUENCE   123 AA;  14356 MW;  CB91870E7B1EB82A CRC64;

  Query Match             87.7%;  Score 554;  DB 1;  Length 123;
  Best Local Similarity   82.1%;  Pred. No. 2.1e-48;
  Matches  101;  Conservative   17;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           |:||:| |||||| |:::|||||||:||:|||||||:||||:||||||||||||||||||
Db       1 MTTLANLTQTLEDAFKKVFITYMDSWRRNTTAEQQALQARVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           :||:|||||||||||||| ||||||||||||:||:||||:||:||||||||:|| ||
Db      61 AFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILHLEDSKATIHENLGATGFT 120

Qy     121 MSP 123
           :||
Db     121 VSP 123


RESULT 3
MINK_HUMAN
ID   MINK_HUMAN     STANDARD;      PRT;   129 AA.
AC   P15382;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89273632; PubMed=2730656;
RA   Murai T., Kakizuka A., Takumi T., Ohkubo H., Nakanishi S.;
RT   "Molecular cloning and sequence analysis of human genomic DNA
RT   encoding a novel membrane protein which exhibits a slowly activating
RT   potassium channel activity.";
RL   Biochem. Biophys. Res. Commun. 161:176-181(1989).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANT GLY-38.
RC   TISSUE=Leukocyte;
RX   MEDLINE=95129890; PubMed=7828904;
RA   Lai L.P., Deng C.L., Moss A.J., Kass R.S., Liang C.S.;
RT   "Polymorphism of the gene encoding a human minimal potassium ion
RT   channel (minK).";
RL   Gene 151:339-340(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cornea;
RA   Rae J.L.;
RT   "Delayed rectifier potassium channel subunit from human cornea
RT   epithelium.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   VARIANT ASN-85.
RX   MEDLINE=97055277; PubMed=8899564;
RA   Tesson F., Donger C., Denjoy I., Berthet M., Bennaceur M., Petit C.,
RA   Coumel P., Schwartz K., Guicheney P.;
RT   "Exclusion of KCNE1 (IsK) as a candidate gene for Jervell and
RT   Lange-Nielsen syndrome.";
RL   J. Mol. Cell. Cardiol. 28:2051-2055(1996).
RN   [5]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=97459933; PubMed=9312006;
RA   Chouabe C., Neyroud N., Guicheney P., Lazdunski M., Romey G.,
RA   Barhanin J.;
RT   "Properties of KvLQT1 K+ channel mutations in Romano-Ward and Jervell
RT   and Lange-Nielsen inherited cardiac arrhythmias.";
RL   EMBO J. 16:5472-5479(1997).
RN   [6]
RP   VARIANT LQT5 58-PRO-PRO-59.
RX   MEDLINE=97472471; PubMed=9328483;
RA   Tyson J., Tranebjaerg L., Bellman S., Wren C., Taylor J.F.N.,
RA   Bathen J., Aslaksen B., Soerland S.J., Lund O., Malcolm S.,
RA   Pembrey M., Bhattacharya S., Bitner-Glindzicz M.;
RT   "IsK and KvLQT1: mutation in either of the two subunits of the slow
RT   component of the delayed rectifier potassium channel can cause
RT   Jervell and Lange-Nielsen syndrome.";
RL   Hum. Mol. Genet. 6:2179-2185(1997).
RN   [7]
RP   VARIANTS LQT5 ILE-7 AND ASN-76.
RX   MEDLINE=98016403; PubMed=9354783;
RA   Schulze-Bahr E., Wang Q., Wedekind H., Haverkamp W., Chen Q., Sun Y.,
RA   Rubie C., Hordt M., Towbin J.A., Borggrefe M., Assmann G., Qu X.,
RA   Somberg J.C., Breithardt G., Oberti C., Funke H.;
RT   "KCNE1 mutations cause Jervell and Lange-Nielsen syndrome.";
RL   Nat. Genet. 17:267-268(1997).
RN   [8]
RP   VARIANTS LQT5 LEU-74 AND ASN-76.
RX   MEDLINE=98016422; PubMed=9354802;
RA   Splawski I., Tristani-Firouzi M., Lehmann M.H., Sanguinetti M.C.,
RA   Keating M.T.;
RT   "Mutations in the hminK gene cause long QT syndrome and suppress IKs
RT   function.";
RL   Nat. Genet. 17:338-340(1997).
RN   [9]
RP   VARIANT LQT5 ASN-76.
RX   MEDLINE=98105943; PubMed=9445165;
RA   Duggal P., Vesely M.R., Wattanasirichaigoon D., Villafane J.,
RA   Kaushik V., Beggs A.H.;
RT   "Mutation of the gene for IsK associated with both Jervell and
RT   Lange-Nielsen and Romano-Ward forms of Long-QT syndrome.";
RL   Circulation 97:142-146(1998).
RN   [10]
RP   VARIANTS LQT5 PHE-47; HIS-51; ASN-76 AND ARG-87.
RX   MEDLINE=99330558; PubMed=10400998;
RA   Bianchi L., Shen Z., Dennis A.T., Priori S.G., Napolitano C.,
RA   Ronchetti E., Bryskin R., Schwartz P.J., Brown A.M.;
RT   "Cellular dysfunction of LQT5-minK mutants: abnormalities of IKs, IKr
RT   and trafficking in long QT syndrome.";
RL   Hum. Mol. Genet. 8:1499-1507(1999).
RN   [11]
RP   VARIANTS LQT5 HIS-32; TRP-98 AND THR-127.
RX   MEDLINE=20432616; PubMed=10973849;
RA   Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori S.G.,
RA   Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,
RA   Keating M.T.;
RT   "Spectrum of mutations in long-QT syndrome genes. KVLQT1, HERG, SCN5A,
RT   KCNE1, and KCNE2.";
RL   Circulation 102:1178-1185(2000).
RN   [12]
RP   VARIANT LQT5 ILE-109.
RX   MEDLINE=21546310; PubMed=11692163;
RA   Schulze-Bahr E., Schwarz M., Hauenschild S., Wedekind H., Funke H.,
RA   Haverkamp W., Breithardt W., Pongs O., Isbrandt D., Breithardt G.;
RT   "A novel long-QT 5 gene mutation in the C-terminus (V109I) is
RT   associated with a mild phenotype.";
RL   J. Mol. Med. 79:504-509(2001).
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS.
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN HEART, LUNG, KIDNEY, TESTIS,
CC       OVARIES, SMALL INTESTINE, PERIPHERAL BLOOD LEUKOCYTES. NOT
CC       DETECTED IN PANCREAS, SPLEEN, PROSTATE AND COLON. RESTRICTIVELY
CC       LOCALIZED IN THE APICAL MEMBRANE PORTION OF EPITHELIAL CELLS.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT (BY
CC       SIMILARITY).
CC   -!- DISEASE: DEFECTS IN KCNE1 ARE THE CAUSE OF THE AUTOSOMAL RECESSIVE
CC       JERVELL AND LANGE-NIELSEN SYNDROME (JLNS). JLNS COMPRISES
CC       PROFOUND CONGENITAL SENSORINEURAL DEAFNESS ASSOCIATED WITH
CC       SYNCOPAL EPISODES. THESE ARE CAUSED BY VENTRICULAR TACHYARRHYTHMIA
CC       SECONDARY TO ABNORMAL REPOLARIZATION, MANIFESTED BY A PROLONGED QT
CC       INTERVAL ON THE ELECTROCARDIOGRAM.
CC   -!- DISEASE: DEFECTS IN KCNE1 ARE THE CAUSE OF LONG QT SYNDROME TYPE 5
CC       (LQT5); A FORM OF HEART DISEASE CHARACTERIZED BY CARDIAC
CC       ARRHYTHMIA. MUTANTS FORM CHANNELS THAT OPEN SLOWLY AND CLOSE
CC       RAPIDLY, THEREBY DIMINISHING POTASSIUM CURRENTS.
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   -!- DATABASE: NAME=LQTSdb; NOTE=KCNE1 mutations page;
CC       WWW="http://www.ssi.dk/en/forskning/lqtsdb/kcne1.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M26685; AAA36129.1; -.
DR   EMBL; L33815; AAA63905.1; -.
DR   EMBL; L28168; AAA58418.1; -.
DR   EMBL; AF135188; AAD25096.1; -.
DR   PIR; A32447; A32447.
DR   Genew; HGNC:6240; KCNE1.
DR   MIM; 176261; -.
DR   MIM; 220400; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
```

```
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation; Polymorphism; Disease mutation;
KW   Long QT syndrome.
FT   DOMAIN        1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     66       POTENTIAL.
FT   DOMAIN       67    129       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     102    102       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT   VARIANT       7      7       T -> I (IN LQT5; JLNS).
FT                                /FTId=VAR_008897.
FT   VARIANT      32     32       R -> H (IN LQT5).
FT                                /FTId=VAR_009906.
FT   VARIANT      38     38       S -> G.
FT                                /FTId=VAR_001558.
FT   VARIANT      47     47       V -> F (IN LQT5; JLNS).
FT                                /FTId=VAR_008898.
FT   VARIANT      51     51       L -> H (IN LQT5; JLNS).
FT                                /FTId=VAR_008899.
FT   VARIANT      58     59       TL -> PP (IN LQT5; JLNS).
FT                                /FTId=VAR_001559.
FT   VARIANT      74     74       S -> L (IN LQT5; RWS).
FT                                /FTId=VAR_008900.
FT   VARIANT      76     76       D -> N (IN LQT5; RWS OR JLNS; SUPPRESSES
FT                                KCNQ1 CURRENTS MARKEDLY).
FT                                /FTId=VAR_008901.
FT   VARIANT      85     85       D -> N.
FT                                /FTId=VAR_008902.
FT   VARIANT      87     87       W -> R (IN LQT5; RWS).
FT                                /FTId=VAR_008903.
FT   VARIANT      98     98       R -> W (IN LQT5).
FT                                /FTId=VAR_009907.
FT   VARIANT     109    109       V -> I (IN LQT5; MILD PHENOTYPE;
FT                                SIGNIFICANTLY REDUCED THE WILD-TYPE I(KS)
FT                                CURRENT AMPLITUDE).
FT                                /FTId=VAR_012802.
FT   VARIANT     127    127       P -> T (IN LQT5).
FT                                /FTId=VAR_009908.
SQ   SEQUENCE   129 AA;  14675 MW;  5442D70929D4E87E CRC64;

  Query Match             21.0%;  Score 132.5;  DB 1;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 1.9e-06;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 4
MINK_FELCA
ID   MINK_FELCA     STANDARD;      PRT;   129 AA.
AC   Q9XSP1;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Chen L.-S.K., Cuddy M.;
RT   "Cloning and expression of the cat delayed rectifier minK potassium
RT   channel.";
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS (BY SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U62404; AAD41532.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     66       POTENTIAL.
FT   DOMAIN       67    129       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     102    102       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   129 AA;  14504 MW;  F696A686CFF8DB95 CRC64;

  Query Match             20.6%;  Score 130.5;  DB 1;  Length 129;
  Best Local Similarity   44.3%;  Pred. No. 2.9e-06;
  Matches   27;  Conservative   15;  Mismatches   16;  Indels    3;  Gaps    2;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESK 107
           ||:::::| | |  : |::| ::|||: |||:|||:: ||  | |||| |:  |   ||  |
Db      45 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDTWQEKDKAYLQARVLESYK 104

Qy     108 A 108
           |
Db     105 A 105


RESULT 5
MINK_MOUSE
ID   MINK_MOUSE     STANDARD;      PRT;   129 AA.
AC   P23299;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=92007723; PubMed=1655403;
RA   Honore E., Attali B., Romey G., Heurteaux C., Ricard P., Lesage F.,
RA   Lazdunski M., Barhanin J.;
RT   "Cloning, expression, pharmacology and regulation of a delayed
RT   rectifier K+ channel in mouse heart.";
RL   EMBO J. 10:2805-2811(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92233938; PubMed=1568475;
RA   Lesage F., Attali B., Lazdunski M., Barhanin J.;
RT   "ISK, a slowly activating voltage-sensitive K+ channel.
RT   Characterization of multiple cDNAs and gene organization in the
```

```
RT   mouse.";
RL   FEBS Lett. 301:168-172(1992).
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS (BY SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: RESTRICTIVELY LOCALIZED IN THE APICAL
CC       MEMBRANE PORTION OF EPITHELIAL CELLS.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X60457; CAA42990.1; -.
DR   PIR; S17307; S17307.
DR   PIR; S21135; S21135.
DR   MGD; MGI:96673; Kcne1.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     66       POTENTIAL.
FT   DOMAIN       67    129       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     102    102       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   129 AA;  14578 MW;  E66DF4742300E839 CRC64;

  Query Match          20.3%;  Score 128.5;  DB 1;  Length 129;
  Best Local Similarity  35.0%;  Pred. No. 4.6e-06;
  Matches   36;  Conservative   22;  Mismatches   28;  Indels   17;  Gaps    6;

Qy      26 WRQNTTAEQ--------EALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRR 77
           |::  ||||           | : |::      ||:::::| | |  : |::| ::||:
Db      17 WQE--TAEQGGNVSGLARKSQLRDDSK---LEALYILMVLGFFGFFTLGIMLSYIRSKKL 71

Qy      78 EHSNDPYHQYIVED-WQEKYKS--QILNLEESKAT-IHENIGA 116
           |||:||:: ||  | |||| |:  |   ||  :|  : ||  |
Db      72 EHSHDPFNVYIESDAWQEKGKAVFQARVLESFRACYVIENQAA 114


RESULT 6
MINK_RAT
ID   MINK_RAT       STANDARD;      PRT;   130 AA.
AC   P15383;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=89058617; PubMed=3194754;
RA   Takumi T., Ohkubo H., Nakanishi S.;
RT   "Cloning of a membrane protein that induces a slow voltage-gated
RT   potassium current.";
RL   Science 242:1042-1045(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=90222152; PubMed=2183220;
RA   Folander K., Smith J.S., Antanavage J., Bennett C., Stein R.B.,
RA   Swanson R.;
RT   "Cloning and expression of the delayed-rectifier IsK channel from
RT   neonatal rat heart and diethylstilbestrol-primed rat uterus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:2975-2979(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=90262731; PubMed=2344412;
RA   Pragnell M., Snay K.J., Trimmer J.S., Maclusky N.J., Naftolin F.,
RA   Kaczmarek L.K., Boyle M.B.;
RT   "Estrogen induction of a small, putative K+ channel mRNA in rat
RT   uterus.";
RL   Neuron 4:807-812(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91035347; PubMed=2229022;
RA   Iwai M., Masu M., Tsuchida K., Mori T., Ohkubo H., Nakanishi S.;
RT   "Characterization of gene organization and generation of
RT   heterogeneous mRNA species of rat ISK protein.";
RL   J. Biochem. 108:200-206(1990).
RN   [5]
RP   MUTAGENESIS OF SER RESIDUES.
RX   MEDLINE=92205350; PubMed=1553557;
RA   Busch A.E., Varnum M.D., North R.A., Adelman J.P.;
RT   "An amino acid mutation in a potassium channel that prevents
RT   inhibition by protein kinase C.";
RL   Science 255:1705-1707(1992).
RN   [6]
RP   MUTAGENESIS OF ASP-77.
RX   MEDLINE=95329285; PubMed=7605639;
RA   Wang K.-W., Goldstein S.A.N.;
RT   "Subunit composition of minK potassium channels.";
RL   Neuron 14:1303-1309(1995).
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS (BY SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: RESTRICTIVELY LOCALIZED IN THE APICAL
CC       MEMBRANE PORTION OF EPITHELIAL CELLS.
CC   -!- INDUCTION: BY ESTROGEN.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT.
CC   -!- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE CARRIED OUT BY
CC       EXPRESSING IN XENOPUS OOCYTES MINK MUTANT EITHER INDIVIDUALLY
CC       (HOMOMULTIMERS) OR IN COMBINATION WITH WILD-TYPE MINK
CC       (HETEROMULTIMERS) IN A 1:1 RATIO.
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M22412; AAA41822.1; -.
DR   EMBL; M36461; AAA41098.1; -.
DR   EMBL; D10709; BAA01553.1; ALT_SEQ.
DR   PIR; A35633; A35633.
DR   PIR; JH0140; JH0140.
DR   PIR; A33177; A33177.
```

```
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     44       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     45     67       POTENTIAL.
FT   DOMAIN       68    130       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     103    103       PHOSPHORYLATION (BY PKC) (PROBABLE).
FT   MUTAGEN      77     77       D->N: NO CURRENT (HOMOMULTIMERS); ONE
FT                                FOURTH OF THE WT CURRENT
FT                                (HETEROMULTIMERS).
SQ   SEQUENCE   130 AA;  14699 MW;  76717E7ED73C5E4D CRC64;

  Query Match             20.3%;  Score 128;  DB 1;  Length 130;
  Best Local Similarity   41.4%;  Pred. No. 5.2e-06;
  Matches   29;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    3;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESK 107
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:  |   ||  :
Db      46 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDAWQEKGKALFQARVLESFR 105

Qy     108 AT-IHENIGA 116
           |  : ||  |
Db     106 ACYVIENQAA 115


RESULT 7
MINK_PIG
ID   MINK_PIG       STANDARD;      PRT;   130 AA.
AC   Q9TUH9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Coronary artery;
RA   Ohya S., Imaizumi Y.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A-POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS (BY SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB032575; BAA86982.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     44       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     45     67       POTENTIAL.
FT   DOMAIN       68    130       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     103    103       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   130 AA;  14671 MW;  76717E7ED724E91D CRC64;

  Query Match             20.2%;  Score 127.5;  DB 1;  Length 130;
  Best Local Similarity   42.6%;  Pred. No. 5.9e-06;
  Matches   26;  Conservative   16;  Mismatches   16;  Indels    3;  Gaps    2;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESK 107
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:  |   ||  :
Db      46 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDAWQEKGKALFQARVLESFR 105

Qy     108 A 108
           |
Db     106 A 106


RESULT 8
MINK_CAVPO
ID   MINK_CAVPO     STANDARD;      PRT;   125 AA.
AC   Q60409; Q9QVZ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=94089666; PubMed=8265583;
RA   Varnum M.D., Busch A.E., Bond C.T., Maylie J., Adelman J.P.;
RT   "The min K channel underlies the cardiac potassium current IKs and
RT   mediates species-specific responses to protein kinase C.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:11528-11532(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart muscle;
RX   MEDLINE=94173910; PubMed=7510407;
RA   Zhang J., Jurkiewicz N.K., Folander K., Lazarides E., Salata J.J.,
RA   Swanson R.;
RT   "K+ currents expressed from the guinea pig cardiac IsK protein are
RT   enhanced by activators of protein kinase C.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:1766-1770(1994).
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS (BY SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
```

```
DR   EMBL; L20462; AAA72394.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     43       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     44     66       POTENTIAL.
FT   DOMAIN       67    125       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     15     17       TVW -> SVM (IN REF. 1).
SQ   SEQUENCE   125 AA;  14266 MW;  E5CB6843D9AB5E76 CRC64;

  Query Match             20.0%;  Score 126.5;  DB 1;  Length 125;
  Best Local Similarity   44.9%;  Pred. No. 7.1e-06;
  Matches   22;  Conservative   15;  Mismatches   11;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS 98
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:
Db      45 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDTWQEKDKA 93


RESULT 9
MINK_RABIT
ID   MINK_RABIT     STANDARD;      PRT;   130 AA.
AC   Q28705;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   IsK slow voltage-gated potassium channel protein (Minimal potassium
DE   channel) (MinK).
GN   KCNE1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand white;
RA   Fermini B., Jurkiewicz N.K., Jow B., Guinosso P., Folander K.,
RA   Swanson R., Salata J.J.;
RT   "Evidence of the slow component of the cardiac delayed rectifier
RT   K+ current (IKs) in rabbit ventricular myocytes.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX. KCNE1 CO-ASSEMBLE WITH KCNQ1
CC       (KVLQT1) TO FORM THE SLOWLY ACTIVATING DELAYED RECTIFIER CARDIAC
CC       POTASSIUM (IKS) CHANNEL. THE OUTWARD CURRENT REACHS ITS STEADY
CC       STATE ONLY AFTER 50 SECONDS (BY SIMILARITY).
CC   -!- SUBUNIT: ASSOCIATES WITH KCNQ1 (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: PHOSPHORYLATION INHIBITS THE POTASSIUM CURRENT (BY
CC       SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L41659; AAA93505.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     44       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     45     67       POTENTIAL.
FT   DOMAIN       68    130       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     103    103       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   130 AA;  14617 MW;  E7B10048F41E205E CRC64;

  Query Match             19.8%;  Score 125;  DB 1;  Length 130;
  Best Local Similarity   34.2%;  Pred. No. 1e-05;
  Matches   25;  Conservative   20;  Mismatches   16;  Indels   12;  Gaps    3;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYI-VEDWQEK----YKSQILN--- 102
           ||:::::| | |  : |::| ::|:: |||:||:: ||   |||||    :::::|
Db      46 LYILMVLGFFGFFTLGIMLSYIRSQKLEHSHDPFNVYIEANDWQEKDRAYFQARVLESCR 105

Qy     103 ----LEESKATIH 111
               ||   | |
Db     106 GCYVLENQLAVEH 118


RESULT 10
YZ04_METJA
ID   YZ04_METJA     STANDARD;      PRT;   439 AA.
AC   Q60260;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein MJECL04.
GN   MJECL04.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanocaldococcaceae; Methanocaldococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   -!- SIMILARITY: SOME, TO M.JANNASCHII MJ0425.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L77118; AAC37078.1; -.
DR   TIGR; MJECL04; -.
DR   InterPro; IPR004256; DUF234.
DR   InterPro; IPR004309; DUF238.
DR   Pfam; PF03008; DUF234; 1.
DR   Pfam; PF03075; DUF238; 1.
KW   Hypothetical protein; ATP-binding; Complete proteome.
FT   NP_BIND      28     35       ATP (POTENTIAL).
SQ   SEQUENCE   439 AA;  52421 MW;  AA50918A58EFC354 CRC64;

  Query Match             13.4%;  Score 84.5;  DB 1;  Length 439;
  Best Local Similarity   23.3%;  Pred. No. 0.43;
  Matches   24;  Conservative   19;  Mismatches   31;  Indels   29;  Gaps    3;

Qy      33 EQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREH------------ 79
           | :||  |:|: || ::::|    ||     : ::       : |||
Db       8 ELKALNEKLDSNNFEFIVIYGRRRIGKTKLALKSV-------ENREHIYYLAVEGDNLKH 60
```

```
Qy      80 ------SNDPYHQYIVEDWQEKY---KSQILNLEESKATIHEN 113
                 :|  :|  |||:  :   | :|: ::|    | ||
Db      61 FKRYASKVEPTIEYAKEDWEAYFNFLKDKIIIIDEFPNLIKEN 103


RESULT 11
CPS_CLOTM
ID   CPS_CLOTM      STANDARD;      PRT;   557 AA.
AC   Q02929;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Putative sensory transducer protein.
OS   Clostridium thermocellum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1515;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCIB 10682;
RX   MEDLINE=93171873; PubMed=8436949;
RA   Hazlewood G.P., Davidson K., Laurie J.I., Huskisson N.S.,
RA   Gilbert H.J.;
RT   "Gene sequence and properties of CelI, a family E endoglucanase from
RT   Clostridium thermocellum.";
RL   J. Gen. Microbiol. 139:307-316(1993).
CC   -!- FUNCTION: MAY BIND ATTRACTANTS OR DETECT CHANGES IN THE
CC       EXTRACELLULAR CONCENTRATION OF SOLUBLE SUGARS.
CC   -!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04736; AAA20891.1; -.
DR   PIR; B47704; B47704.
DR   HSSP; P02942; 1QU7.
DR   InterPro; IPR004089; Chmtaxis_transd.
DR   InterPro; IPR003660; HAMP.
DR   Pfam; PF00015; MCPsignal; 1.
DR   Pfam; PF00672; HAMP; 1.
DR   SMART; SM00304; HAMP; 1.
DR   SMART; SM00283; MA; 1.
KW   Chemotaxis; Transducer; Transmembrane; Methylation.
FT   TRANSMEM    122    145       POTENTIAL.
FT   MOD_RES     268    268       DEAMIDATION AND METHYLATION (BY
FT                                SIMILARITY).
FT   MOD_RES     274    274       METHYLATION (BY SIMILARITY).
FT   MOD_RES     281    281       DEAMIDATION AND METHYLATION
FT                                (BY SIMILARITY).
FT   MOD_RES     463    463       METHYLATION (BY SIMILARITY).
SQ   SEQUENCE   557 AA;  61042 MW;  169875A91F614446 CRC64;

  Query Match             12.1%;  Score 76.5;  DB 1;  Length 557;
  Best Local Similarity   23.2%;  Pred. No. 3.5;
  Matches   29;  Conservative   24;  Mismatches   47;  Indels   25;  Gaps    5;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           :| : :   || | |   |: |      |||| :| :       :    :: ::: :|:
Db      84 LSDIDDIGDTLRDYF-EAFVEY------NTTAAKEKVDENKQVASTASTVMIVVIFVGIL 136

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYI----------VE-DWQEKYKSQILNLEESKAT 109
             | : : :| : ||       |  | :          || | : : : :|  | ||
Db     137 IAIALGVFISRIISK-------PIGQMVEAADRLALGDVEVDVKAETRDEIGKLAESFKR 189

Qy     110 IHENI 114
           : |||
Db     190 MIENI 194


RESULT 12
MIR2_HUMAN
ID   MIR2_HUMAN     STANDARD;      PRT;   103 AA.
AC   Q9Y6H6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Minimum potassium ion channel-related peptide 2 (MiRP2) (MinK-related
DE   peptide 2).
GN   KCNE3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Abbott G.W., Sesti F., Buck M.E., Goldstein S.A.N.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ANCILLARY PROTEIN THAT CO-ASSEMBLE WITH A POTASSIUM
CC       CHANNEL ALPHA-SUBUNIT TO MODULATE THE GATING KINETICS AND ENHANCE
CC       STABILITY OF THE MULTIMERIC COMPLEX (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE KCNE FAMILY OF POTASSIUM CHANNELS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF076531; AAD28089.1; -.
DR   Genew; HGNC:6243; KCNE3.
DR   MIM; 604433; -.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Glycoprotein.
FT   DOMAIN       1     57       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    58     78       POTENTIAL.
FT   DOMAIN      79    103       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    41     41       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   103 AA;  11710 MW;  5235385E8D08BF10 CRC64;

  Query Match             12.0%;  Score 76;  DB 1;  Length 103;
  Best Local Similarity   30.0%;  Pred. No. 0.6;
  Matches   18;  Conservative   16;  Mismatches   22;  Indels    4;  Gaps    2;

Qy      29 NTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYI 88
             | | |: |     | :| |  ||::|    :|:  : ::::   :|:: :  :|||| ||
Db      41 NQTEERRASLPGRD-DNSYMYILFVMF---LFAVTVGSLILGYTRSRKVDKRSDPYHVYI 96


RESULT 13
SYI_BORBU
ID   SYI_BORBU      STANDARD;      PRT;  1042 AA.
AC   O51773;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
DE   (IleRS).
GN   ILES OR BB0833.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OC   Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35210 / B31;
RX   MEDLINE=98065943; PubMed=9403685;
RA   Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
```

```
RA   Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA   Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA   Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA   van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA   Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA   Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA   Smith H.O., Venter J.C.;
RT   "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT   burgdorferi.";
RL   Nature 390:580-586(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP +
CC       diphosphate + L-isoleucyl-tRNA(Ile).
CC   -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE001181; AAC67179.1; -.
DR   HSSP; P56690; 1ILE.
DR   TIGR; BB0833; -.
DR   InterPro; IPR002300; tRNA-synt_1a.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   InterPro; IPR002301; tRNA-synt_ile.
DR   Pfam; PF00133; tRNA-synt_1; 1.
DR   PRINTS; PR00984; TRNASYNTHILE.
DR   TIGRFAMs; TIGR00392; ileS; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW   Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW   Metal-binding; Zinc; Complete proteome.
FT   SITE         48     58       "HIGH" REGION.
FT   SITE        594    598       "KMSKS" REGION.
FT   BINDING     597    597       ATP (BY SIMILARITY).
SQ   SEQUENCE   1042 AA;  122331 MW;  6C0F7D820CA32F75 CRC64;

  Query Match             11.8%;  Score 74.5;  DB 1;  Length 1042;
  Best Local Similarity   27.3%;  Pred. No. 11;
  Matches   33;  Conservative   24;  Mismatches   45;  Indels   19;  Gaps    8;

Qy       6 NFTQTLEDVFRRIFITYMDNW------RQNTTAEQEALQAKVDA-ENFYYVILYLMVMIG 58
           | |:::| :    ||  ::||      |:   :| :  : | || |  || |  ||:::
Db     703 NLTKSIESLLE--FIDKLNNWYIRRSRRRFWKSEND--KDKNDAYETLYYAIKTLMILLA 758

Qy      59 MF-SFIIVAIL--VSTVKSKRREHSND---PYHQYIVEDWQEKYK--SQILNLEESKATI 110
            |  ||   |   : | : |:  | ||       :| :  :||     :| ::  |  ::
Db     759 PFIPFITEEIYQNLKTDEDKQSIHLNDYPKANENFINKTIEEKINLARKITSMARSLRSL 818

Qy     111 H 111
           |
Db     819 H 819


RESULT 14
V120_HSV7J
ID   V120_HSV7J     STANDARD;      PRT;   938 AA.
AC   P52438;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Capsid assembly protein U30.
GN   U30.
OS   Human herpesvirus (type 7 / strain JI) (HHV7).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=57278;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Nicholas J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
CC       EHV-1 23, EBV BOLF1, VZV 21, HVS-1 63, AND HCMV UL47.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U43400; AAC54692.1; -.
KW   Capsid assembly.
SQ   SEQUENCE   938 AA;  110170 MW;  F4E39A2BF0D32BC9 CRC64;

  Query Match             11.7%;  Score 74;  DB 1;  Length 938;
  Best Local Similarity   27.0%;  Pred. No. 11;
  Matches   30;  Conservative   19;  Mismatches   56;  Indels    6;  Gaps    4;

Qy       3 TLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSF 62
           || ||   :| :      || |           :|     :|  |||  |     :|:|
Db     773 TLQNFIIIVERISSHANTTYQDVLNSIDECHFSNMQLIQSFKNIVYVIDVLNTK-NIFNF 831

Qy      63 IIVAILVSTVKSKRREHSNDPYHQY-IVEDWQEKYKSQILNL-EESKATIH 111
             : : |:   |  :::   | |:|  : :|:    || : || |: | ||:
Db     832 SLASQLIEAKKLVKKQ---DTYNQLNVQDDFVTVLKSHLNNLFEKQKPTIN 879


RESULT 15
NU2M_CHOCR
ID   NU2M_CHOCR     STANDARD;      PRT;   497 AA.
AC   P48903;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
GN   ND2 OR NAD2.
OS   Chondrus crispus (Carragheen).
OG   Mitochondrion.
OC   Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinaceae;
OC   Chondrus.
OX   NCBI_TaxID=2769;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Apices;
RX   MEDLINE=95341681; PubMed=7616569;
RA   Leblanc C., Boyen C., Richard O., Bonnard G., Grienenberger J.M.,
RA   Kloareg B.;
RT   "Complete sequence of the mitochondrial DNA of the rhodophyte
RT   Chondrus crispus (Gigartinales). Gene content and genome
RT   organization.";
RL   J. Mol. Biol. 250:484-495(1995).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC       inner membrane.
CC   -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z47547; CAA87619.1; -.
DR   InterPro; IPR001750; Oxidored_q1.
DR   Pfam; PF00361; oxidored_q1; 1.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ   SEQUENCE   497 AA;  56853 MW;  DB00BF38039F40CA CRC64;
```

Query Match 11.6%; Score 73.5; DB 1; Length 497;
Best Local Similarity 26.2%; Pred. No. 6.2;
Matches 16; Conservative 14; Mismatches 14; Indels 17; Gaps 2;

```
Qy      43 AENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN 102
           : : :|||:|:: |:|:||||:                |  ||      :| :|   :::
Db     335 SSSIFYVIIYVITMLGIFSFILTL----------RFYNYSYH------YQTRYLQDLIS 377

Qy     103 L 103
           |
Db     378 L 378
```

Search completed: May 15, 2003, 14:23:21
Job time : 15 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 14:22:29 ; Search time 30 Seconds
(without alignments)
844.793 Million cell updates/sec

Title: US-09-550-163-2
Perfect score: 632
Sequence: 1 MSTLSNFTQTLEDVFRRIFI.....EESKATIHENIGAAGFKMSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560	88.6	123	11	Q9D808	Q9d808 mus musculu
2	553	87.5	123	11	Q8R1Z7	Q8r1z7 mus musculu
3	354	56.0	71	6	Q9BDR0	Q9bdr0 oryctolagus
4	132.5	21.0	129	11	Q91Z94	Q91z94 cavia porce
5	97	15.3	57	6	Q9N100	Q9n100 sus scrofa
6	80.5	12.7	43	11	O35438	O35438 meriones un
7	78.5	12.4	568	16	Q9CKR9	Q9ckr9 pasteurella
8	75.5	11.9	367	16	Q9JYH3	Q9jyh3 neisseria m
9	75.5	11.9	4065	3	Q9P4Z1	Q9p4z1 neurospora
10	75	11.9	1003	16	Q8YPF5	Q8ypf5 anabaena sp
11	73.5	11.6	171	12	Q69504	Q69504 human herpe
12	73.5	11.6	652	3	O74974	O74974 schizosacch
13	73	11.6	170	4	Q8WWG9	Q8wwg9 homo sapien
14	73	11.6	591	16	Q8YTH8	Q8yth8 anabaena sp
15	73	11.6	1224	5	O96209	O96209 plasmodium
16	72.5	11.5	237	11	Q9CUV2	Q9cuv2 mus musculu
17	72.5	11.5	371	16	Q99SL2	Q99sl2 staphylococ
18	72.5	11.5	437	2	O33587	O33587 staphylococ
19	72	11.4	844	5	Q966J3	Q966j3 caenorhabdi
20	71.5	11.3	361	5	Q19083	Q19083 caenorhabdi
21	71.5	11.3	895	5	Q8T9C0	Q8t9c0 drosophila
22	71.5	11.3	899	5	Q9V7B6	Q9v7b6 drosophila
23	71.5	11.3	1013	2	Q9L953	Q9l953 streptococc
24	71.5	11.3	1386	8	Q9XMS2	Q9xms2 tetrahymena
25	71	11.2	84	12	Q8V3J9	Q8v3j9 swinepox vi
26	71	11.2	174	16	Q8YRL6	Q8yrl6 anabaena sp
27	71	11.2	1877	10	Q9ZNW4	Q9znw4 sorghum bic
28	70.5	11.2	451	17	Q9V0D7	Q9v0d7 pyrococcus
29	70.5	11.2	455	17	Q8TH19	Q8th19 pyrococcus
30	70	11.1	170	4	Q96CC4	Q96cc4 homo sapien
31	70	11.1	522	16	Q99QY7	Q99qy7 staphylococ
32	70	11.1	546	5	Q22453	Q22453 caenorhabdi
33	70	11.1	947	16	P95022	P95022 mycobacteri
34	70	11.1	5388	5	Q9U1D0	Q9u1d0 leishmania
35	69.5	11.0	188	16	Q8XJW8	Q8xjw8 clostridium
36	69.5	11.0	198	5	Q9NNV9	Q9nnv9 plasmodium
37	69.5	11.0	554	5	Q23508	Q23508 caenorhabdi
38	69.5	11.0	693	10	Q9SR87	Q9sr87 arabidopsis
39	69.5	11.0	932	3	P89499	P89499 saccharomyc
40	69.5	11.0	1154	3	O74755	O74755 schizosacch
41	69.5	11.0	3973	5	O96204	O96204 plasmodium
42	69	10.9	282	16	O31856	O31856 bacillus su
43	69	10.9	359	16	Q931S3	Q931s3 staphylococ
44	69	10.9	548	16	Q99UC9	Q99uc9 staphylococ
45	69	10.9	773	10	Q98RM5	Q98rm5 guillardia

ALIGNMENTS

RESULT 1
Q9D808
ID Q9D808 PRELIMINARY; PRT; 123 AA.
AC Q9D808;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 2200002I16Rik protein.
GN 2200002I16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008619; BAB25781.1; -.
DR MGD; MGI:1916393; 2200002I16Rik.

```
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR01605; KCNE2CHANNEL.
DR   PRINTS; PR00168; KCNECHANNEL.
SQ   SEQUENCE   123 AA;  14348 MW;  0A5DB7759BFD741C CRC64;

  Query Match             88.6%;  Score 560;  DB 11;  Length 123;
  Best Local Similarity   84.6%;  Pred. No. 7.3e-51;
  Matches  104;  Conservative   14;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
          |:||:| |||||| |::|||||||:||:|||||::||||:||||||||||||||||||||
Db      1 MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAENFYYVILYLMVMIGMF 60

Qy     61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
          |||:||||||||||||||| ||||||||||||||||||:||:||||||||:|| ||
Db     61 SFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQEKYKSQILHLEDSKATIHENMGATGFT 120

Qy    121 MSP 123
          :||
Db    121 VSP 123


RESULT 2
Q8R1Z7
ID   Q8R1Z7      PRELIMINARY;      PRT;   123 AA.
AC   Q8R1Z7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   RIKEN cDNA 2200002I16 gene.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EYE;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022699; AAH22699.1; -.
SQ   SEQUENCE   123 AA;  14370 MW;  0A52784967FD741C CRC64;

  Query Match             87.5%;  Score 553;  DB 11;  Length 123;
  Best Local Similarity   83.7%;  Pred. No. 3.9e-50;
  Matches  103;  Conservative   14;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
          |:||:| |||||| |::|||||||:||:|||||::||||:||||||||||||||||||||
Db      1 MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAENFYYVILYLMVMIGMF 60

Qy     61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
          |||:|||||||||||||  ||||||||||||||||||:||:||||||||:|| ||
Db     61 SFIVVAILVSTVKSKRREHSQHPYHQYIVEDWQEKYKSQILHLEDSKATIHENMGATGFT 120

Qy    121 MSP 123
          :||
Db    121 VSP 123


RESULT 3
Q9BDR0
ID   Q9BDR0      PRELIMINARY;      PRT;    71 AA.
AC   Q9BDR0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   K+/pacemaker channel beta subunit MiRP1 (Fragment).
GN   KCNE2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wymore R.T., Holmes B.A., Wymore R.S., Yu H., Wu J., Potapova I.,
RA   Zuckerman J., Pan Z., Wang H., Shi W., Robinson R., El-Maghrabi R.,
RA   Benjamin W., Dixon J.E., McKinnon D., Cohen I.S.;
RT   "Mirp1: A beta subunit for the HCN ion channel family enhances
RT   expression and speeds kinetics.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF329636; AAK15527.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR00168; KCNECHANNEL.
FT   NON_TER       1      1
FT   NON_TER      71     71
SQ   SEQUENCE   71 AA;  8557 MW;  4A667539D4032CEA CRC64;

  Query Match             56.0%;  Score 354;  DB 6;  Length 71;
  Best Local Similarity   95.8%;  Pred. No. 1.3e-29;
  Matches   68;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     43 AENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db      1 AENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILH 60

Qy    103 LEESKATIHEN 113
          ||:|||||||
Db     61 FEEAKATIHEN 71


RESULT 4
Q91Z94
ID   Q91Z94      PRELIMINARY;      PRT;   129 AA.
AC   Q91Z94;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Potassium voltage-gated channel IsK-related family member 1.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Jiang M., Zhang M., Liu J., Tseng G.-N.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY050512; AAL13162.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR01604; KCNE1CHANNEL.
SQ   SEQUENCE   129 AA;  14645 MW;  4843171C7DC1A92A CRC64;

  Query Match             21.0%;  Score 132.5;  DB 11;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 3.2e-06;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy     51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
          ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db     45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 5
Q9N100
ID   Q9N100      PRELIMINARY;      PRT;    57 AA.
AC   Q9N100;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   KCNE1 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Li Y., Freeman L.C.;
RT   "PKC modulation of granulosa IKs does not involve a PKC site in pig
RT   minK.";
RL   Biophys. J. 78:208A-208A(2000).
DR   EMBL; AF233358; AAF43426.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
DR   PRINTS; PR01604; KCNE1CHANNEL.
DR   PRINTS; PR00168; KCNECHANNEL.
FT   NON_TER       1      1
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6726 MW;  EFB66FD93473ACF6 CRC64;

  Query Match             15.3%;  Score 97;  DB 6;  Length 57;
  Best Local Similarity   44.6%;  Pred. No. 0.0067;
  Matches   25;  Conservative   11;  Mismatches   16;  Indels    4;  Gaps    3;

Qy      65 VAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESKAT-IHENIGA 116
           : |::| ::||: |||:|||: ||  | |||| |:  |   ||  :|  : ||  |
Db       2 LGIMLSYIRSKKLEHSHDPYNVYIQSDSWQEKDKAYFQARVLENCRACYVIENQAA 57


RESULT 6
O35438
ID   O35438      PRELIMINARY;      PRT;    43 AA.
AC   O35438;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   K+ channel subunit IsK (Fragment).
GN   ISK.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART, VESTIBULAR LABYRINTH, AND STRIA VASCULARIS;
RX   MEDLINE=98097798; PubMed=9435509;
RA   Marcus D.C., Sunose H., Liu J., Shen Z., Scofield M.A.;
RT   "P2U purinergic receptor inhibits apical IsK/KvLQT1 channel via
RT   protein kinase C in vestibular dark cells.";
RL   Am. J. Physiol. 273:C2022-C2029(1997).
DR   EMBL; AF029765; AAB84214.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   Pfam; PF02060; ISK_Channel; 1.
KW   Ionic channel.
FT   NON_TER       1      1
FT   NON_TER      43     43
SQ   SEQUENCE   43 AA;  5062 MW;  D6C5C230C87D4869 CRC64;

  Query Match             12.7%;  Score 80.5;  DB 11;  Length 43;
  Best Local Similarity   47.5%;  Pred. No. 0.26;
  Matches   19;  Conservative    7;  Mismatches   11;  Indels    3;  Gaps    2;

Qy      72 VKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESKA 108
           ::||: |||:|||: ||  | || | |:  |   ||  :|
Db       2 IRSKKLEHSHDPYNVYIESDAWQAKGKAVFQARVLESCRA 41


RESULT 7
Q9CKR9
ID   Q9CKR9      PRELIMINARY;      PRT;   568 AA.
AC   Q9CKR9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HsdM.
GN   HSDM OR PM1537.
OS   Pasteurella multocida.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Pasteurella.
OX   NCBI_TaxID=747;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PM70;
RX   MEDLINE=21145866; PubMed=11248100;
RA   May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT   "Complete genomic sequence of Pasteurella multocida Pm70.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR   EMBL; AE006190; AAK03621.1; -.
DR   InterPro; IPR003665; Methylase_M.
DR   InterPro; IPR002296; N12N6_mtfrase.
DR   InterPro; IPR003356; N6_DNA_Mtase.
DR   Pfam; PF02506; Methylase_M; 1.
DR   Pfam; PF02384; N6_Mtase; 1.
DR   PRINTS; PR00507; N12N6MTFRASE.
KW   Complete proteome.
SQ   SEQUENCE   568 AA;  65503 MW;  29163A09A446C741 CRC64;

  Query Match             12.4%;  Score 78.5;  DB 16;  Length 568;
  Best Local Similarity   26.4%;  Pred. No. 7;
  Matches   29;  Conservative   21;  Mismatches   31;  Indels   29;  Gaps    6;

Qy      23 MDNWRQNTTAEQEA--------LQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKS 74
           |:|  |    | :|        |:: ::| |: :||| |: :     ::  | |
Db       1 MNNSEQQYLNELDAKLWKSADKLRSNIEAANYKHVILSLIFL----KYVSDAFLA----- 51

Qy      75 KRREHS-----NDPYHQYIVE----DWQEKYKSQILN-LEESKATIHENI 114
             |:||      || | | ::    | :|:|:  : | ||:      ||:
Db      52 --RQHSIQQQLTDPEHLYYLDPSFYDSEEEYQQALANELEQLDYYTEENV 99


RESULT 8
Q9JYH3
ID   Q9JYH3      PRELIMINARY;      PRT;   367 AA.
AC   Q9JYH3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Protease, putative.
GN   NMB1587.
OS   Neisseria meningitidis (serogroup B).
OC   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX   NCBI_TaxID=491;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MC58 / SEROGROUP B;
RX   MEDLINE=20175755; PubMed=10710307;
RA   Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA   Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA   Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA   Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA   Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
RA   Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA   Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA   Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT   "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT   MC58.";
RL   Science 287:1809-1815(2000).
DR   EMBL; AE002509; AAF41940.1; -.
DR   MEROPS; S49.002; -.
DR   TIGR; NMB1587; -.
DR   InterPro; IPR002142; Peptidase_U7.
DR   Pfam; PF01343; Peptidase_U7; 1.
DR   ProDom; PD002897; Peptidase_U7; 1.
KW   Complete proteome.
SQ   SEQUENCE   367 AA;  41414 MW;  814711B59F2C6684 CRC64;

  Query Match             11.9%;  Score 75.5;  DB 16;  Length 367;
  Best Local Similarity   29.8%;  Pred. No. 9;
  Matches   25;  Conservative   17;  Mismatches   25;  Indels   17;  Gaps    4;
```

```
Qy      33 EQEALQA--KVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVE 90
           ||| :|:  |    |:   :| |: : |  : |::||    |:||::  |       ::
Db      11 EQEEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAI----VQSKKQSESG----SVVLT 62

Qy      91 DWQEKYKSQ-------ILNLEESK 107
           |: | || |        |: ||:|
Db      63 DFSENYKKQRQSFEAFFLSGEEAK 86


RESULT 9
Q9P4Z1
ID   Q9P4Z1      PRELIMINARY;      PRT;  4065 AA.
AC   Q9P4Z1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Related to TOM1 protein.
GN   B11B22.010.
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   German Neurospora genome project;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL356834; CAB92704.2; -.
DR   InterPro; IPR000569; HECT_domain.
DR   Pfam; PF00632; HECT; 2.
DR   SMART; SM00119; HECTc; 2.
DR   PROSITE; PS50237; HECT; 2.
SQ   SEQUENCE   4065 AA;  452568 MW;  F74683CEC36F9350 CRC64;

  Query Match           11.9%;  Score 75.5;  DB 3;  Length 4065;
  Best Local Similarity  24.6%;  Pred. No. 1.2e+02;
  Matches   29;  Conservative   21;  Mismatches   49;  Indels   19;  Gaps    3;

Qy       6 NFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIV 65
           |  |  ||   |:: |  :       : :  :  :|||      ||  :   |   ::
Db    2937 NAEQQAEDERPRVYYTLRNQ-------QIDITELGIDAE-------YLEALPEEFRDEVI 2982

Qy      66 AILVSTVKSKRREH-----SNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAG 118
           |  :|| :|: ||       |    |  :|   |: :::||: |: :    |   |||
Db    2983 AQAISTRRSQAREQVSQEGENTEVFQEFLEALPEELRNEILHQEQHEQRRRERQNAAG 3040


RESULT 10
Q8YPF5
ID   Q8YPF5      PRELIMINARY;      PRT;  1003 AA.
AC   Q8YPF5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Toxin secretion ABC transporter ATP-binding protein.
GN   ALR4239.
OS   Anabaena sp. (strain PCC 7120).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=103690;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21595285; PubMed=11759840;
RA   Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA   Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA   Yasuda M., Tabata S.;
RT   "Complete genomic sequence of the filamentous nitrogen-fixing
RT   cyanobacterium Anabaena sp. strain PCC 7120.";
RL   DNA Res. 8:205-213(2001).
DR   EMBL; AP003595; BAB75938.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001950; TIF_SUI1.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   ProDom; PD000006; ABC_transportr; 1.
DR   SMART; SM00382; AAA; 1.
DR   SMART; SM00100; cNMP; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR   PROSITE; PS50042; CNMP_BINDING_3; 1.
DR   PROSITE; PS01118; SUI1_1; UNKNOWN_1.
KW   ATP-binding; Complete proteome.
SQ   SEQUENCE   1003 AA;  111718 MW;  1260643429D6C6FA CRC64;

  Query Match           11.9%;  Score 75;  DB 16;  Length 1003;
  Best Local Similarity  23.0%;  Pred. No. 30;
  Matches   31;  Conservative   20;  Mismatches   30;  Indels   54;  Gaps    7;

Qy      20 ITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVM---------IGMFS---FIIVAI 67
           |  ::| ||  |    ||  :||   : ::|::||         :|: :   |||: :
Db     548 INELENIRQFLTG--TALTVGLDA---VFSVVYIIVMLFYSWQLTLVGLGTIPIFIIITL 602

Qy      68 LVSTVKSKR---REHSNDPYHQYIVE------------------DWQEKYKSQILNLEE 105
           : |   |::   :   |     |:||                  |||:|   :
Db     603 IASPTVSRQLRSKAERNSETQSYLVEVMSGIQTVKAQNIELRSRFSWQERYARYV----- 657

Qy     106 SKATIHENIGAAGFK 120
                  |||||
Db     658 ----------AAGFK 662


RESULT 11
Q69504
ID   Q69504      PRELIMINARY;      PRT;   171 AA.
AC   Q69504;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   U23 protein.
GN   U23.
OS   Human herpesvirus (type 7 / strain JI) (HHV7).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=57278;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JI;
RA   Nicholas J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RK;
RA   Megaw A.G., Rapaport D., Avidor B., Frenkel N., Davison A.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RK;
RA   Megaw A.G., Frenkel N., Davison A.J.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U43400; AAC54684.1; -.
DR   EMBL; AF037218; AAC40736.1; -.
SQ   SEQUENCE   171 AA;  18663 MW;  ADE85FA5909D8C20 CRC64;

  Query Match           11.6%;  Score 73.5;  DB 12;  Length 171;
  Best Local Similarity  36.6%;  Pred. No. 6.3;
  Matches   15;  Conservative   11;  Mismatches   12;  Indels    3;  Gaps    1;

Qy      50 ILYLMVMIGMFSFI---IVAILVSTVKSKRREHSNDPYHQY 87
```

```
          :|:|:::|   |||    :|:||  :|: :| ||  | : |
Db    121 VLFLVILIAAVSFIGIVALALLVLLIKNPKRNHSKKPKNAY 161


RESULT 12
O74974
ID   O74974      PRELIMINARY;      PRT;   652 AA.
AC   O74974;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 75.7 kDa protein.
GN   SPCC1827.01C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Seeger K., Harris D, Wood V., Rajandream M.A., Barrell B.G.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL023777; CAA19309.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   652 AA;  75651 MW;  96BB732F2273DE6B CRC64;

  Query Match            11.6%;  Score 73.5;  DB 3;  Length 652;
  Best Local Similarity   22.0%;  Pred. No. 27;
  Matches   22;  Conservative   19;  Mismatches   30;  Indels   29;  Gaps    2;

Qy      23 MDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSND 82
           |::  :|   ||||:|  :: |:                        |:  : :: | |
Db      65 MEDENENENDEQEAIQYYINVES-------------------QDADETLHQEAQDSSED 104

Qy      83 PYHQYIVEDWQEKYKSQIL---------NLEESKATIHEN 113
           |:||:   |  |  |: |          ::|||  : ::
Db     105 PFHQHFDYDDSEVIKNSIAAYDEGKLCKSIEESKLGVSQS 144


RESULT 13
Q8WWG9
ID   Q8WWG9      PRELIMINARY;      PRT;   170 AA.
AC   Q8WWG9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Potassium voltage-gated channel-like protein.
GN   KCNE4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY, AND HEART;
RA   Hui R., Teng S., Lin C., Ma L., Zhen Y.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY065987; AAL49979.1; -.
DR   InterPro; IPR000369; ISK_Channel.
DR   PRINTS; PR00168; KCNECHANNEL.
SQ   SEQUENCE   170 AA;  18397 MW;  1C6FBCF87298F6C0 CRC64;

  Query Match            11.6%;  Score 73;  DB 4;  Length 170;
  Best Local Similarity   27.7%;  Pred. No. 7.1;
  Matches   23;  Conservative   16;  Mismatches   34;  Indels   10;  Gaps    3;

Qy      23 MDNWRQNTTAEQEALQAKVDA-----ENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRR 77
           :::    | |    |:::         | |: || :|   |:|   :: |::  :|||||
Db       7 LNSTHPGTAASSSPLESRAAGGGSGNGNEYFYILVVMSFYGIF---LIGIVLGYMKSKRR 63

Qy      78 EHSNDPYHQYIVED--WQEKYKS 98
           |  :     |  |:  | |  ||
Db      64 EKKSSLLLLYKDEERLWGEAMKS 86


RESULT 14
Q8YTH8
ID   Q8YTH8      PRELIMINARY;      PRT;   591 AA.
AC   Q8YTH8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Two-component sensor histidine kinase.
GN   ALR2739.
OS   Anabaena sp. (strain PCC 7120).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=103690;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21595285; PubMed=11759840;
RA   Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA   Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA   Yasuda M., Tabata S.;
RT   "Complete genomic sequence of the filamentous nitrogen-fixing
RT   cyanobacterium Anabaena sp. strain PCC 7120.";
RL   DNA Res. 8:205-213(2001).
DR   EMBL; AP003590; BAB74438.1; -.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR004358; Bact_sens_pr_C.
DR   InterPro; IPR003660; HAMP.
DR   InterPro; IPR003661; His_kinA.
DR   InterPro; IPR004359; HIS_KIN_sig.
DR   Pfam; PF00672; HAMP; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; signal; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
DR   SMART; SM00304; HAMP; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
KW   Kinase; Complete proteome.
SQ   SEQUENCE   591 AA;  67107 MW;  B328BB6D2696C5D2 CRC64;

  Query Match            11.6%;  Score 73;  DB 16;  Length 591;
  Best Local Similarity   21.3%;  Pred. No. 28;
  Matches   30;  Conservative   22;  Mismatches   35;  Indels   54;  Gaps    6;

Qy       4 LSNFTQT----LEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFY---------YVI 50
           :::| |     || : :|             | || :  : | || |          |
Db     138 INSFNQDIQLFLEQIIQR-------------AYQERILLEQDLENLYQVQRIISIVVVA 183

Qy      51 LYLMVMIGMFSFIIVAILVSTVKS-----------------KRREHSNDPYHQYIVEDW 92
           : ||:|| |    : |   |:||                  :   |: |      :||
Db     184 VILMLLIGKF----ILIWQPTIKSIQNLQLGTAEIAAGNFDYRLNIHTGDE-----IEDL 234

Qy      93 QEKYKSQILNLEESKATIHEN 113
           : :    : | :|: |: :|
Db     235 AQAFNDMAVKLSQSRETLMKN 255


RESULT 15
O96209
ID   O96209      PRELIMINARY;      PRT;  1224 AA.
AC   O96209;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Hypothetical 144.0 kDa protein.
GN   PFB0580W.
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99021743; PubMed=9804551;
RA   Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
RA   Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
RA   Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
RA   Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA   Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT   "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT   falciparum.";
RL   Science 282:1126-1132(1998).
DR   EMBL; AE001404; AAC71905.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1224 AA;  144031 MW;  B585BB28D47BDC3F CRC64;

  Query Match             11.6%;  Score 73;  DB 5;  Length 1224;
  Best Local Similarity   18.6%;  Pred. No. 61;
  Matches   13;  Conservative   23;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      36 ALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEK 95
           :: | |   ||  :: ||    |:    :: : :|: : : ::: |  |::| :::  ::
Db    1001 SVAAYVQINNFLNLVYYLSNSYGIILAKLIGVYISSQRKREKDNQNKKYNEYNLKEPMKE 1060

Qy      96 YKSQILNLEE 105
           |   :   |
Db    1061 YTKLFVEKNE 1070


Search completed: May 15, 2003, 14:26:13
Job time : 34 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 14:25:44 ; Search time 53 Seconds
(without alignments)
223.839 Million cell updates/sec

Title: US-09-550-163-2
Perfect score: 632
Sequence: 1 MSTLSNFTQTLEDVFRRIFI.....EESKATIHENIGAAGFKMSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	632	100.0	123	9	US-10-000-151B-4	Sequence 4, Appli
2	632	100.0	123	10	US-09-864-761-49007	Sequence 49007, A
3	533	84.3	103	10	US-09-864-761-36713	Sequence 36713, A
4	132.5	21.0	76	10	US-09-864-761-37234	Sequence 37234, A
5	132.5	21.0	129	9	US-10-138-316-4	Sequence 4, Appli
6	70	11.1	523	10	US-09-815-242-5723	Sequence 5723, Ap
7	70	11.1	525	10	US-09-815-242-12651	Sequence 12651, A
8	68.5	10.8	1590	9	US-10-180-326-1	Sequence 1, Appli
9	67.5	10.7	380	10	US-09-134-333-12	Sequence 12, Appl
10	67	10.6	272	10	US-09-815-242-5572	Sequence 5572, Ap
11	67	10.6	277	10	US-09-815-242-12282	Sequence 12282, A
12	66.5	10.5	380	10	US-09-134-333-13	Sequence 13, Appl
13	65.5	10.4	553	10	US-09-815-242-5778	Sequence 5778, Ap
14	65.5	10.4	1276	10	US-09-982-610-24	Sequence 24, Appl
15	65.5	10.4	2016	9	US-09-896-994-2	Sequence 2, Appli
16	65.5	10.4	2016	10	US-09-840-125-4	Sequence 4, Appli
17	65	10.3	367	10	US-09-815-242-10676	Sequence 10676, A
18	65	10.3	1482	10	US-09-815-242-12484	Sequence 12484, A
19	65	10.3	1835	10	US-09-935-541-5	Sequence 5, Appli
20	65	10.3	2175	10	US-09-935-541-2	Sequence 2, Appli
21	65	10.3	2188	10	US-09-935-541-4	Sequence 4, Appli
22	64.5	10.2	425	9	US-10-174-590-570	Sequence 570, App
23	64.5	10.2	425	9	US-10-176-758-570	Sequence 570, App
24	64.5	10.2	425	9	US-10-175-737-570	Sequence 570, App
25	64.5	10.2	425	9	US-10-173-706-570	Sequence 570, App
26	64.5	10.2	425	9	US-10-175-738-570	Sequence 570, App
27	64.5	10.2	425	9	US-10-175-752-570	Sequence 570, App
28	64.5	10.2	425	9	US-10-176-482-570	Sequence 570, App
29	64.5	10.2	425	9	US-10-176-757-570	Sequence 570, App
30	64.5	10.2	425	9	US-10-176-913-570	Sequence 570, App
31	64.5	10.2	425	9	US-10-180-552-570	Sequence 570, App
32	64.5	10.2	425	9	US-10-180-557-570	Sequence 570, App
33	64.5	10.2	425	9	US-10-173-700-570	Sequence 570, App
34	64.5	10.2	425	9	US-10-174-572-570	Sequence 570, App
35	64.5	10.2	425	9	US-10-174-579-570	Sequence 570, App
36	64.5	10.2	425	9	US-10-174-582-570	Sequence 570, App
37	64.5	10.2	425	9	US-10-174-588-570	Sequence 570, App
38	64.5	10.2	425	9	US-10-175-739-570	Sequence 570, App
39	64.5	10.2	425	9	US-10-175-740-570	Sequence 570, App
40	64.5	10.2	425	9	US-10-175-743-570	Sequence 570, App
41	64.5	10.2	425	9	US-10-176-488-570	Sequence 570, App
42	64.5	10.2	425	9	US-10-176-492-570	Sequence 570, App
43	64.5	10.2	425	9	US-10-176-747-570	Sequence 570, App
44	64.5	10.2	425	9	US-10-176-750-570	Sequence 570, App
45	64.5	10.2	425	9	US-10-176-985-570	Sequence 570, App

ALIGNMENTS

RESULT 1
US-10-000-151B-4
; Sequence 4, Application US/10000151B
; Publication No. US20030013136A1
; GENERAL INFORMATION:
; APPLICANT: Balser, Jeffrey R.
; APPLICANT: George, Alfred L.
; TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
; FILE REFERENCE: Vanderbilt Ref No. US20030013136A1 VU0120; Attorney Docket No. US2
; CURRENT APPLICATION NUMBER: US/10/000,151B
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-151B-4

Query Match 100.0%; Score 632; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.9e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123
```

RESULT 2
US-09-864-761-49007
; Sequence 49007, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

```
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 49007
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000120.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.67
;   OTHER INFORMATION: EST_HUMAN HIT: AI962650.1, EVALUE 3.00e-59
;   OTHER INFORMATION: SWISSPROT HIT: Q9Y6J6, EVALUE 7.00e-67
US-09-864-761-49007

  Query Match           100.0%;  Score 632;  DB 10;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-61;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123
```

```
RESULT 3
US-09-864-761-36713
; Sequence 36713, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36713
;   LENGTH: 103
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000052.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.88
;   OTHER INFORMATION: SWISSPROT HIT: Q9Y6J6, EVALUE 2.00e-55
;   OTHER INFORMATION: EST_HUMAN HIT: AI962650.1, EVALUE 1.00e-54
US-09-864-761-36713
```

```
  Query Match             84.3%;  Score 533;  DB 10;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-50;
  Matches  103;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      19 FITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRRE 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 FITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRRE 60

Qy      79 HSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFKM 121
           |||||||||||||||||||||||||||||||||||||||||||
Db      61 HSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFKM 103


RESULT 4
US-09-864-761-37234
; Sequence 37234, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37234
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000121.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
;   OTHER INFORMATION: EST_HUMAN HIT: AI246239.1, EVALUE 2.00e-07
;   OTHER INFORMATION: SWISSPROT HIT: P15382, EVALUE 1.00e-39
US-09-864-761-37234

  Query Match             21.0%;  Score 132.5;  DB 10;  Length 76;
  Best Local Similarity   45.1%;  Pred. No. 2.8e-07;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db       9 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 59


RESULT 5
US-10-138-316-4
; Sequence 4, Application US/10138316
; Publication No. US20030054380A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-162
;  CURRENT APPLICATION NUMBER: US/10/138,316
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/444,295
;  PRIOR FILING DATE: 1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-316-4

  Query Match             21.0%;  Score 132.5;  DB 9;  Length 129;
  Best Local Similarity   45.1%;  Pred. No. 5.4e-07;
  Matches   23;  Conservative   15;  Mismatches   12;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
           ||:::::| | |  : |::| ::||: ||||||:: ||  | |||| |: :
Db      45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95


RESULT 6
US-09-815-242-5723
; Sequence 5723, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
```

```
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5723
;   LENGTH: 523
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-5723

  Query Match             11.1%;  Score 70;  DB 10;  Length 523;
  Best Local Similarity   27.9%;  Pred. No. 18;
  Matches   29;  Conservative   14;  Mismatches   33;  Indels   28;  Gaps    5;

Qy      35 EALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQ 93
           ||::| |:||              | | || :    |   :   :  ::||: |: |  |
Db      44 EAIEAIVEAE------------GRFDFIYIQAPYSETLTNLLQMISEPYNTYVDESFWS 90

Qy      94 ---------EKYKSQIL---NLEE--SKATIHENIGAAGFKMSP 123
                  :||  | |   |:||  :|       |  | |:||
Db      91 VEYEQDENVQKYVVQPLHYRNIEERNNKLEAVSFSGQYGDKVSP 134


RESULT 7
US-09-815-242-12651
; Sequence 12651, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12651
;   LENGTH: 525
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-12651

  Query Match             11.1%;  Score 70;  DB 10;  Length 525;
  Best Local Similarity   27.9%;  Pred. No. 18;
  Matches   29;  Conservative   14;  Mismatches   33;  Indels   28;  Gaps    5;

Qy      35 EALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQ 93
           ||::| |:||              | | || :    |   :   :  ::||: |: |  |
Db      46 EAIEAIVEAE------------GRFDFIYIQAPYSETLTNLLQMISEPYNTYVDESFWS 92

Qy      94 ---------EKYKSQIL---NLEE--SKATIHENIGAAGFKMSP 123
                  :||  | |   |:||  :|       |  | |:||
Db      93 VEYEQDENVQKYVVQPLHYRNIEERNNKLEAVSFSGQYGDKVSP 136


RESULT 8
US-10-180-326-1
; Sequence 1, Application US/10180326
; Publication No. US20030049661A1
; GENERAL INFORMATION:
;  APPLICANT: Seino, Susumu
;  APPLICANT:  Shibasaki, Tadao
;  APPLICANT:  Ozaki, No. US20030049661Aluaki
;  TITLE OF INVENTION: Protein Rim2
;  FILE REFERENCE: P21573
;  CURRENT APPLICATION NUMBER: US/10/180,326
;  CURRENT FILING DATE:  2002-06-27
;  PRIOR APPLICATION NUMBER: JP 288372/99
;  PRIOR FILING DATE: 1999-10-08<160>  5
;  NUMBER OF SEQ ID NOS:
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1590
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-180-326-1

  Query Match             10.8%;  Score 68.5;  DB 9;  Length 1590;
  Best Local Similarity   23.9%;  Pred. No. 1e+02;
  Matches   28;  Conservative   19;  Mismatches   57;  Indels   13;  Gaps    3;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           |  ||: |:  |:  |:| :  ||  ::    ||  |: | :          :       |
Db      26 MPDLSHLTE--EE--RKIILAVMDRQKKEEEKEQSVLKIKEE---------HKAQPTQWF 72

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAA 117
             |  :  ||: |   :::  |:   |  :    | || |:  : |       |  | |
Db      73 PFSGITELVNNVLQPQQKQPNEKEPQTKLHQQFEMYKEQVKKMGEESQQQQEQKGDA 129


RESULT 9
US-09-134-333-12
; Sequence 12, Application US/09134333
; Patent No. US20020076403A1
; GENERAL INFORMATION:
;  APPLICANT: LONGACRE-ANDRE, SHIRLEY
;  APPLICANT: ROTH, CHARLES
;  APPLICANT: NATO, FARIDABANO
;  APPLICANT: BARNWELL, JOHN
;  APPLICANT: MENDIS, KAMINI
;  TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
;  TITLE OF INVENTION: PLASMODIUM MSP-1
;  FILE REFERENCE: 0660-0135-0XCIP
;  CURRENT APPLICATION NUMBER: US/09/134,333
;  CURRENT FILING DATE: 1999-04-18
;  EARLIER APPLICATION NUMBER: PCT/FR97/00290
```

```
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: FR96/01822
;  EARLIER FILING DATE: 1996-02-14
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Plasmodium vivax-like sp.
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 1-140-REGION I
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 141-178-REGION II
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 179-283-REGION III
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 284-380-REGION IV
US-09-134-333-12

  Query Match             10.7%;  Score 67.5;  DB 10;  Length 380;
  Best Local Similarity   24.4%;  Pred. No. 22;
  Matches   31;  Conservative   17;  Mismatches   28;  Indels   51;  Gaps    6;

Qy      28 QNTT--AEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSN---- 81
           | ||  || || :  | |    | ::||  : ||:          |:| :   | |
Db       2 QVTTGEAESEAPEILVPAGISDYDVVYLKPLAGMY---------KTIKKQLENHVNAFNT 52

Qy      82 ----------------------------DPYHQYIVEDWQEKYKSQILNLEESKATI-- 110
                                        |  :||::|    ||  :|:||: |  :
Db      53 NITDMLDSRLKKRNYFLEVLNSDLNPFKYSPSGEYIIKD---PYK--LLDLEKKKKLLGS 107

Qy     111 HENIGAA 117
           :: |||:
Db     108 YKYIGAS 114


RESULT 10
US-09-815-242-5572
; Sequence 5572, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5572
;   LENGTH: 272
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-5572

  Query Match             10.6%;  Score 67;  DB 10;  Length 272;
  Best Local Similarity   20.7%;  Pred. No. 17;
  Matches   31;  Conservative   21;  Mismatches   44;  Indels   54;  Gaps    5;

Qy      12 EDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVST 71
           ||:|    : : |  |:|  |  ||  :::  :   |: |||:   |       |::| |
Db      67 EDLFITSKLYFEDFGRENVAAAYEASLSRLGLK---YLDLYLVHWPGTNE----AVMVDT 119

Qy      72 VKSKRREHSND-----------------------------PYHQY------------- 87
             |     : |:                             || |
Db     120 WKGMEDLYKNNKVKNIGVSNFEPEHLEALLAQVSIKPVINQVEYHPYLTQHKLKLYLAAQ 179

Qy      88 --IVEDWQEKYKSQILNLEESKATIHENIG 115
             ::| |     :|||| :|:   | : :|
Db     180 HIVMESWSPLMNAQILN-DETIKDIAQELG 208


RESULT 11
US-09-815-242-12282
; Sequence 12282, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12282
;   LENGTH: 277
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-12282

  Query Match             10.6%;  Score 67;  DB 10;  Length 277;
  Best Local Similarity   20.7%;  Pred. No. 17;
  Matches   31;  Conservative   21;  Mismatches   44;  Indels   54;  Gaps    5;

Qy      12 EDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVST 71
           ||:|    : : |  |:|  |  ||  :::  :   |: |||:   |       |::| |
Db      71 EDLFITSKLYFEDFGRENVAAAYEASLSRLGLK---YLDLYLVHWPGTNE----AVMVDT 123

Qy      72 VKSKRREHSND-----------------------------PYHQY------------- 87
             |     : |:                             || |
Db     124 WKGMEDLYKNNKVKNIGVSNFEPEHLEALLAQVSIKPVINQVEYHPYLTQHKLKLYLAAQ 183

Qy      88 --IVEDWQEKYKSQILNLEESKATIHENIG 115
```

```
           ::| |     :|||| :|:   | : :|
Db    184 HIVMESWSPLMNAQILN-DETIKDIAQELG 212


RESULT 12
US-09-134-333-13
; Sequence 13, Application US/09134333
; Patent No. US20020076403A1
; GENERAL INFORMATION:
;  APPLICANT: LONGACRE-ANDRE, SHIRLEY
;  APPLICANT: ROTH, CHARLES
;  APPLICANT: NATO, FARIDABANO
;  APPLICANT: BARNWELL, JOHN
;  APPLICANT: MENDIS, KAMINI
;  TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF
;  TITLE OF INVENTION: PLASMODIUM MSP-1
;  FILE REFERENCE: 0660-0135-0XCIP
;  CURRENT APPLICATION NUMBER: US/09/134,333
;  CURRENT FILING DATE: 1999-04-18
;  EARLIER APPLICATION NUMBER: PCT/FR97/00290
;  EARLIER FILING DATE: 1997-02-14
;  EARLIER APPLICATION NUMBER: FR96/01822
;  EARLIER FILING DATE: 1996-02-14
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Plasmodium vivax-like sp.
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 1-140-REGION I
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 141-178-REGION II
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 179-283-REGION III
;   FEATURE:
;   OTHER INFORMATION: Amino Acids 284-380-REGION IV
US-09-134-333-13

  Query Match             10.5%;  Score 66.5;  DB 10;  Length 380;
  Best Local Similarity   25.2%;  Pred. No. 29;
  Matches   32;  Conservative   18;  Mismatches   26;  Indels   51;  Gaps    7;

Qy      28 QNTT--AEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSN---- 81
           | ||  || || :  | |    | ::||  : ||:          |:| :   | |
Db       2 QVTTGEAESEAPEILVPAGISDYDVVYLKPLAGMY---------KTIKKQLENHVNAFNT 52

Qy      82 ------------------------DPYH-----QYIVEDWQEKYKSQILNLEESKATI-- 110
                                    :|:      :||::|    ||  :|:||: |  |
Db      53 NITDMLDSRLKKRNYFLEVLNSDLNPFKYSSSGEYIIKD---PYK--LLDLEKKKKLIGS 107

Qy     111 HENIGAA 117
           :: |||:
Db     108 YKYIGAS 114


RESULT 13
US-09-815-242-5778
; Sequence 5778, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5778
;   LENGTH: 553
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-09-815-242-5778

  Query Match             10.4%;  Score 65.5;  DB 10;  Length 553;
  Best Local Similarity   20.8%;  Pred. No. 59;
  Matches   26;  Conservative   24;  Mismatches   44;  Indels   31;  Gaps    5;

Qy       9 QTLEDVFRRI----FITYMDNWRQNTTAEQEALQAKVDAENFYYVILY------------ 52
           | : ||   |    |   :   | ::  |  |::  |:  |   |  :
Db     190 QDINDVIEAIKNASFPVLLAGMRSSSAEETNAIRKLVERTNLPVVETFQGAGVISRELEN 249

Qy      53 -LMVMIGMF------SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEE 105
              :|:|         :  : ||:|:          ||  :|   :| :: ::||:|::|
Db     250 HFFGRVGLFRNQVGDELLRKSDLVATI-------GYDPI-EYEASNWNKELETQIINIDE 301

Qy     106 SKATI 110
           :| |
Db     302 VQAEI 306


RESULT 14
US-09-982-610-24
; Sequence 24, Application US/09982610
; Patent No. US20020146420A1
;  GENERAL INFORMATION:
;       APPLICANT: Genentech, Inc.
;                  Bennett, Brian D.
;                  Goeddel, David
;                  Lee, James M.
;                  Matthews, William
;                  Tsai, Siao Ping
;                  Wood, William I.
;       TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
;       NUMBER OF SEQUENCES: 45
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/982,610
;            FILING DATE: 17-Oct-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/446,648
;            FILING DATE: 1996-MAY-23
```

```
;             APPLICATION NUMBER: 08/222616
;             FILING DATE: 04-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lee, Wendy M.
;             REGISTRATION NUMBER: 40,378
;             REFERENCE/DOCKET NUMBER: P0821P3PCT
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-1994
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1276 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-982-610-24

  Query Match             10.4%;  Score 65.5;  DB 10;  Length 1276;
  Best Local Similarity   28.2%;  Pred. No. 1.6e+02;
  Matches   31;  Conservative   13;  Mismatches   37;  Indels   29;  Gaps    5;

Qy      24 DNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRRE-HSND 82
           : ||     || || |         |:| |:|       |:||:|    :|  ||   :|
Db     532 EGWR-----EQLALIAGTAVVG---VVLVLVV-------IVVAVLCLRKQSNGREAEYSD 576

Qy      83 PYHQYIV------------EDWQEKYKSQILNLEESKATIHENIGAAGF 119
            : ||::              ||  |  :    :: |   | | |||  |
Db     577 KHGQYLIGHGTKVYIDPFTYEDPNEAVREFAKEIDVSYVKIEEVIGAGEF 626


RESULT 15
US-09-896-994-2
; Sequence 2, Application US/09896994
; Publication No. US20030074024A1
;   GENERAL INFORMATION:
;        APPLICANT: Ken Stokes
;                   Jos e Morissette
;        TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
;                            SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1ris
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/896,994
;             FILING DATE: 02-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/514,907
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Paul K. Legaard
;             REGISTRATION NUMBER: 38,534
;             REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 568-3100
;             TELEFAX: (215) 568-3439
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2016 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: unknown
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-896-994-2

  Query Match             10.4%;  Score 65.5;  DB 9;  Length 2016;
  Best Local Similarity   20.5%;  Pred. No. 2.9e+02;
  Matches   26;  Conservative   27;  Mismatches   43;  Indels   31;  Gaps    6;

Qy       4 LSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFI 63
             |: |    :| : |::              |: |::   |   | :   |:: :|  ||
Db     363 LALFRLMTQDCWERLY-------------QQTLRS---AGKIYMIFFMLVIFLG--SFY 403

Qy      64 IVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYK-----SQILNLEESKATIH--ENIGA 116
           :| :::: |     |      :|  : : :|| |      ::|  |    ||   : :
Db     404 LVNLILAVVAMAYEEQ-----NQATIAETEEKEKRFQEAMEMLKKEHEALTIRGVDTVSR 458

Qy     117 AGFKMSP 123
           :  :|||
Db     459 SSLEMSP 465


Search completed: May 15, 2003, 14:35:09
Job time : 73 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 14:16:39 ; Search time 76 Seconds
(without alignments)
215.656 Million cell updates/sec

Title: US-09-550-163-2
Perfect score: 632
Sequence: 1 MSTLSNFTQTLEDVFRRIFI.....EESKATIHENIGAAGFKMSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	632	100.0	123	21	AAB29585	Human potassium ch
2	632	100.0	123	22	AAM78528	Human protein SEQ
3	632	100.0	123	22	AAM18627	Peptide #5061 enco
4	632	100.0	123	22	AAM06194	Peptide #4876 enco
5	632	100.0	123	22	AAB67800	Amino acid sequenc
6	632	100.0	123	22	AAU00215	Human potassium ch
7	632	100.0	123	23	AAU99168	Human ether-a-go-g
8	632	100.0	123	23	AAE22095	Human MiRP1 wild t
9	632	100.0	135	22	ABB11948	Human MiRP1 homolo
10	632	100.0	135	22	AAM79512	Human protein SEQ
11	629	99.5	123	21	AAB29593	Human potassium ch
12	628	99.4	123	23	AAE22094	Human MiRP1 mutant
13	627	99.2	123	21	AAB29595	Human potassium ch
14	627	99.2	123	21	AAB29596	Human potassium ch
15	627	99.2	123	23	AAE22097	Human MiRP1 mutant
16	627	99.2	123	23	AAE22098	Human MiRP1 mutant
17	626	99.1	123	21	AAB29594	Human potassium ch
18	626	99.1	123	23	AAE22096	Human MiRP1 mutant
19	554	87.7	123	21	AAB29586	Rat potassium chan
20	554	87.7	123	22	AAU00216	Rat potassium chan
21	533	84.3	103	22	ABB30832	Peptide #3483 enco
22	533	84.3	103	22	ABB36009	Peptide #3515 enco
23	533	84.3	103	22	ABB21415	Protein #3414 enco
24	533	84.3	103	22	AAM56804	Human brain expres
25	533	84.3	103	22	AAM69184	Human bone marrow
26	533	84.3	103	22	AAM17016	Peptide #3450 enco
27	533	84.3	103	22	AAM29508	Peptide #3545 enco
28	533	84.3	103	22	AAM04723	Peptide #3405 enco
29	533	84.3	103	23	ABG38787	Human peptide enco
30	132.5	21.0	76	22	ABB36597	Peptide #4103 enco
31	132.5	21.0	76	22	ABB21936	Protein #3935 enco
32	132.5	21.0	76	22	AAM57360	Human brain expres
33	132.5	21.0	76	22	AAM17576	Peptide #4010 enco
34	132.5	21.0	76	22	AAM30099	Peptide #4136 enco
35	132.5	21.0	76	23	ABG39383	Human peptide enco
36	132.5	21.0	129	21	AAY57369	Human KCNE1 protei
37	132.5	21.0	129	21	AAY80563	Human long QT synd
38	132.5	21.0	129	22	AAE00622	Human cardiac pota
39	132.5	21.0	129	22	AAU00218	Human potassium ch
40	132.5	21.0	129	22	AAB49498	Human minK. Homo
41	132.5	21.0	132	16	AAR65160	Potassium ion chan
42	128	20.3	130	11	AAR06612	Intracellular pota
43	127.5	20.2	129	22	AAE00623	Human cardiac pota
44	126	19.9	130	22	AAU00217	Rat potassium chan
45	76.5	12.1	368	21	AAY74262	Neisseria gonorrhe

ALIGNMENTS

RESULT 1
AAB29585
ID AAB29585 standard; Protein; 123 AA.
XX
AC AAB29585;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human potassium channel protein KCNE2 (MiRP1), SEQ ID NO:2.
XX
KW Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW MinK-related; long QT syndrome; cardiac arrhythmia;
KW drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW HERG.
XX
OS Homo sapiens.
XX
PN WO200063434-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10004.
XX
PR 15-APR-1999; 99US-0129404.
XX
PA (UTAH) UNIV UTAH RES FOUND.
PA (UYYA) UNIV YALE.
XX
PI Abbott GW, Sesti F, Splawski I, Keating MT, Goldstein SAN;
XX
DR WPI; 2000-672747/65.
DR N-PSDB; AAC64071.

XX
PT Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT diagnosing and treating ion channel disorders, especially long QT
PT syndrome -
XX
PS Claim 19; Page 119; 132pp; English.
XX
CC The invention relates to novel ion channel proteins related to
CC KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC respectively). The cDNAs encoding these proteins are given in AAC64071-
CC AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC potassium channels (I-KR), mutations in which are associated with long
CC QT syndrome. The invention also relates to methods of diagnosing long QT
CC syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC nonhuman animals comprising a heterologous ion channel protein gene
CC of the invention, a transgenic animal comprising human KNCE2 and HERG
CC DNA, and methods of and screening drugs for treating long QT syndrome
CC using KCNE2 proteins (including mutants), nucleic acids encoding them
CC and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC acids, and proteins may be used for diagnosing or treating ion channel
CC disorders, especially long QT syndrome. Transgenic animals comprising
CC KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC The present sequence represents human KCNE2 (MiRP1).
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 632; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-67;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy     61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy    121 MSP 123
          |||
Db    121 MSP 123
```

RESULT 2
AAM78528
ID AAM78528 standard; Protein; 123 AA.
XX
AC AAM78528;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1190.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK51661.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 3438-3439; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 632; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-67;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy     61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy    121 MSP 123
          |||
Db    121 MSP 123
```

RESULT 3
AAM18627
ID AAM18627 standard; Protein; 123 AA.
XX
AC AAM18627;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #5061 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX

```
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 27; SEQ ID No 23453; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC   by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC   can be used to produce a single exon microarray, which can be used for
CC   measuring human gene expression in a sample derived from human cervical
CC   epithelial cells. By measuring gene expression, the probes are therefore
CC   useful in grading and/or staging of diseases of the cervix, notably
CC   cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   123 AA;

  Query Match             100.0%;  Score 632;  DB 22;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-67;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 4
AAM06194
ID   AAM06194 standard; Protein; 123 AA.
XX
AC   AAM06194;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Peptide #4876 encoded by probe for measuring breast gene expression.
XX
KW   Probe; human; breast disease; breast cancer; development disorder;
KW   inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS   Homo sapiens.
XX
PN   WO200157270-A2.
XX
PD   09-AUG-2001.
XX
PF   29-JAN-2001; 2001WO-US00661.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-476286/51.
XX
PT   Novel single exon nucleic acid probe used to measuring gene expression
PT   in a human breast -
XX
PS   Claim 27; SEQ ID No 14934; 322pp; English.
XX
CC   The present invention relates to novel single exon nucleic acid probes
CC   (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC   such probe. The probes are useful for measuring human gene expression in
CC   a human breast sample, where the probe hybridises at high stringency to a
CC   nucleic acid expressed in the human breast. The probes are useful for
CC   predicting, diagnosing, grading, staging, monitoring and prognosing
CC   diseases of the human breast, particularly those diseases with polygenic
CC   aetiology. The diseases include: breast cancer, disorders of development,
CC   inflammatory diseases of the breast, fibrocystic changes, proliferative
CC   breast disease and non-carcinoma tumours.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   123 AA;

  Query Match             100.0%;  Score 632;  DB 22;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-67;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 5
AAB67800
ID   AAB67800 standard; Protein; 123 AA.
XX
AC   AAB67800;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of human potassium channel subunit IsK2.
XX
KW   Human; potassium channel; IsK2; gene therapy; gastric motility;
KW   gastric acid secretion; anti-arrhythmic agent; myocardial infarction.
XX
OS   Homo sapiens.
XX
PN   WO200127246-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-US28014.
XX
```

PR 12-OCT-1999; 99US-0158781.
XX
PA (MERI) MERCK & CO INC.
XX
PI Swanson RJ, Liu Y, Folander K;
XX
DR WPI; 2001-273764/28.
DR N-PSDB; AAF80269.
XX
PT New DNA encoding the IsK2 potassium channel subunit, useful e.g. for
PT detecting mutations and screening for therapeutic agents -
XX
PS Claim 8; Fig 1B; 46pp; English.
XX
CC The present sequence represents a human potassium channel subunit,
CC designated IsK2. The IsK2 polynucleotide, and derived probes, are
CC used diagnostically to detect mutations in the IsK2 gene, to determine
CC levels of mRNA expression and to isolate homologous sequences; for
CC recombinant expression of IsK2; in gene therapy to increase potassium
CC channel activity and to generate transgenic animals, as models and
CC for drug screening. Recombinant IsK2 is used for studying biochemical
CC activity of IsK2 and its role in disorders of gastric motility and
CC gastric acid secretion, and to raise specific antibodies. IsK2
CC modulators are potentially useful for treating diseases associated with
CC increased or reduced potassium channel activity, e.g. as
CC anti-arrhythmic agents for treating myocardial infarction and as
CC regulators of gastric acid secretion.
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 632; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-67;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
Db 1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy 61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
Db 61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy 121 MSP 123
Db 121 MSP 123

RESULT 6
AAU00215
ID AAU00215 standard; Protein; 123 AA.
XX
AC AAU00215;
XX
DT 10-MAY-2001 (first entry)
XX
DE Human potassium channel regulatory protein, MINK2.
XX
KW Human; MINK2; potassium channel; cardiac arrhythmia; hypertension;
KW angina; asthma; diabetes; renal insufficiency; urinary incontinence;
KW irritable colon; epilepsy; cerebrovascular ischaemia; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200114403-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US22799.
XX
PR 20-AUG-1999; 99US-0379201.
XX
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Ficker E, Wible B, Brown AM;
XX
DR WPI; 2001-218424/22.
DR N-PSDB; AAS00245.
XX
PT Novel potassium channel gene termed MinK2 encoding potassium channel
PT regulatory protein, useful for screening compounds that are useful for
PT treating diseases caused by aberrant potassium activity -
XX
PS Disclosure; Fig 9; 39pp; English.
XX
CC The sequence represents the amino acid sequence of human potassium
CC channel regulatory protein, MINK2. MINK2 sequence is useful for producing
CC a potassium channel regulatory protein useful for in vitro or in vivo
CC screening of agonistic or antagonistic compounds that are useful for
CC treating diseases caused by aberrant potassium activity, such as human
CC cardiac arrhythmias, hypertension, angina, asthma, diabetes, renal
CC insufficiency, urinary incontinence, irritable colon, epilepsy,
CC cerebrovascular ischaemia, and autoimmune disease.
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 632; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-67;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
Db 1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy 61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
Db 61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy 121 MSP 123
Db 121 MSP 123

RESULT 7
AAU99168
ID AAU99168 standard; Protein; 123 AA.
XX
AC AAU99168;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human ether-a-go-go related interacting protein MiRP1.
XX
KW Human; human ether-a-go-go related gene; HERG; KCR1; MiRP1;
KW long QT syndrome; LQT; single nucleotide polymorphism; cardiac arrythmia;
KW potassium channel.
XX
OS Homo sapiens.
XX
PN WO200242735-A2.
XX
PD 30-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US45644.
XX
PR 30-OCT-2000; 2000US-244340P.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Balser JR, George AL, Roden DM;
XX
DR WPI; 2002-527650/56.
DR N-PSDB; ABK86573.
XX
PT Identifying a potassium channel activity modulator for drug design,
PT comprises contacting a compound with a potassium channel and rat
PT cerebellar cDNA library (KCR1) polypeptide, and determining activity -

```
XX
PS   Disclosure; Page 163; 164pp; English.
XX
CC   The invention relates to identifying (M1) a compound that modulates
CC   biological activity of a potassium channel (PC), by contacting a
CC   compound with a structure comprising a PC polypeptide and a polypeptide
CC   cloned from a rat cerebellar cDNA library (KCR1), and determining the
CC   activity of the PC polypeptide in the presence and absence of the
CC   compound, where a difference in the activities indicates modulation of
CC   biological activity of PC. Also include are identifying (M2) a candidate
CC   compound that modulates the biological activity of a complex comprising a
CC   human ether-a-go-go-related gene (HERG) channel polypeptide and a KCR1
CC   polypeptide, identifying (M3) a candidate compound as a modulator of KCR1
CC   expression, modulating (M4) PC function in a subject, comprising
CC   administering to the subject a substance that provides expression of a
CC   KCR1-encoding nucleic acid molecule in a cell or tissue, where modulated
CC   PC function is desired, screening (M5) for susceptibility to a drug-
CC   induced cardiac arrhythmia in a subject, comprising obtaining a
CC   biological sample from the subject and detecting a polymorphism of a KCR1
CC   gene in the biological sample from the subject, where the presence of the
CC   polymorphism indicates the susceptibility of the subject to a
CC   drug-induced cardiac arrhythmia, an oligonucleotide pair, where a first
CC   oligonucleotide of the pair hybridises to a first portion of a KCR1 gene
CC   which includes a polymorphism of the KCR1 gene, and the second
CC   oligonucleotide of the pair hybridises to a second portion of the KCR1
CC   gene that is adjacent to the first portion and a set of antisense
CC   oligonucleotide primers, suitable for amplifying a portion of a KCR1 gene
CC   which includes a polymorphism of the KCR1 gene. (M1) is useful for
CC   identifying a compound that modulates biological activity of PC,
CC   especially HERG, for modulating PC function (i.e modulating HERG
CC   activity) in a mammal, by preparing a composition comprising the
CC   compound and administering the composition. The compound is useful for
CC   treating or preventing long QT syndrome (LOT) and is useful in drug
CC   designing. The present sequence represents a HERG interacting
CC   protein MiRP1 (not defined).
XX
SQ   Sequence   123 AA;

  Query Match             100.0%;  Score 632;  DB 23;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-67;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 8
AAE22095
ID   AAE22095 standard; Protein; 123 AA.
XX
AC   AAE22095;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human MiRP1 wild type protein.
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia.
XX
OS   Homo sapiens.
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   N-PSDB; AAD35170.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 8; Fig 1A; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human MiRP1 wild type protein.
XX
SQ   Sequence   123 AA;

  Query Match             100.0%;  Score 632;  DB 23;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-67;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 9
ABB11948
ID   ABB11948 standard; peptide; 135 AA.
XX
AC   ABB11948;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human MiRP1 homologue, SEQ ID NO:2318.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer.
XX
OS   Homo sapiens.
```

XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR N-PSDB; ABA09192.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 20; Page 283; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.
XX
SQ Sequence 135 AA;

Query Match 100.0%; Score 632; DB 22; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 72

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 132

Qy     121 MSP 123
          |||
Db     133 MSP 135
```

RESULT 10
AAM79512
ID AAM79512 standard; Protein; 135 AA.
XX
AC AAM79512;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3158.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52645.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 270; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemiu, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 135 AA;

Query Match 100.0%; Score 632; DB 22; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 72

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 132

Qy     121 MSP 123
           |||
Db     133 MSP 135
```

```
RESULT 11
AAB29593
ID   AAB29593 standard; Protein; 123 AA.
XX
AC   AAB29593;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) mutant Q9E.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   N-PSDB; AAC64083.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents a mutant human KCNE2 (MiRP1)
CC   specifically claimed for use in diagnostic and drug screening methods of
CC   the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 protein sequence shown on page
CC   119.
XX
SQ   Sequence   123 AA;
```

```
  Query Match             99.5%;  Score 629;  DB 21;  Length 123;
  Best Local Similarity   99.2%;  Pred. No. 4.4e-67;
  Matches  122;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTETLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123
```

```
RESULT 12
AAE22094
ID   AAE22094 standard; Protein; 123 AA.
XX
AC   AAE22094;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human MiRP1 mutant protein (A116V).
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 116
FT                   /note= "Wild type Ala substituted with Val"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   N-PSDB; AAD35169.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 1; Page 42; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
```

```
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human MiRP1 mutant protein (A116V).
XX
SQ   Sequence   123 AA;

  Query Match             99.4%;  Score 628;  DB 23;  Length 123;
  Best Local Similarity   99.2%;  Pred. No. 5.8e-67;
  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGVAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 13
AAB29595
ID   AAB29595 standard; Protein; 123 AA.
XX
AC   AAB29595;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) mutant I57T.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   N-PSDB; AAC64085.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents a mutant human KCNE2 (MiRP1)
CC   specifically claimed for use in diagnostic and drug screening methods of
CC   the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 protein sequence shown on page
CC   119.
XX
SQ   Sequence   123 AA;

  Query Match             99.2%;  Score 627;  DB 21;  Length 123;
  Best Local Similarity   99.2%;  Pred. No. 7.6e-67;
  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMTGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 14
AAB29596
ID   AAB29596 standard; Protein; 123 AA.
XX
AC   AAB29596;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) mutant T8A.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   N-PSDB; AAC64086.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
```

```
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents a mutant human KCNE2 (MiRP1)
CC   specifically claimed for use in diagnostic and drug screening methods of
CC   the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 protein sequence shown on page
CC   119.
XX
SQ   Sequence   123 AA;

  Query Match             99.2%;  Score 627;  DB 21;  Length 123;
  Best Local Similarity   99.2%;  Pred. No. 7.6e-67;
  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFAQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


RESULT 15
AAE22097
ID   AAE22097 standard; Protein; 123 AA.
XX
AC   AAE22097;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human MiRP1 mutant protein (I57T).
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 57
FT                   /note= "Wild type Ile substituted with Thr"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   N-PSDB; AAD35172.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 29; Page 46-47; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human MiRP1 mutant protein (I57T).
XX
SQ   Sequence   123 AA;

  Query Match             99.2%;  Score 627;  DB 23;  Length 123;
  Best Local Similarity   99.2%;  Pred. No. 7.6e-67;
  Matches  122;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMTGMF 60

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 SFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAGFK 120

Qy     121 MSP 123
           |||
Db     121 MSP 123


Search completed: May 15, 2003, 14:24:43
Job time : 77 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 19:45:19 ; Search time 596.902 Seconds
(without alignments)
10011.921 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_442
Perfect score: 369
Sequence: 1 atgtctactttatccaattt.....ctgggttcaaaatgtccccc 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	354.8	96.2	803	12	BG208163	BG208163 RST27654
	2	333	90.2	410	9	AI962650	AI962650 wq42e03.x
	3	333	90.2	429	9	AI654552	AI654552 wb48b12.x
	4	328.8	89.1	391	9	AI339609	AI339609 qq42a07.x
	5	325	88.1	372	9	AI246239	AI246239 qi29g04.x
	6	266.6	72.2	1691	11	AK008619	AK008619 Mus muscu
	7	257.8	69.9	470	14	D85797	D85797 D85797 Rat
	8	242	65.6	1003	12	BG261965	BG261965 602373784
	9	177.8	48.2	746	12	BG221966	BG221966 RST41783
	10	168.2	45.6	351	13	BG938225	BG938225 1Abo14A12
	11	157	42.5	188	9	AA633404	AA633404 np69h11.s
	12	119.4	32.4	121	9	AA935321	AA935321 oo71g09.s
c	13	99	26.8	311	10	AW869303	AW869303 MR3-SN006
	14	90	24.4	314	10	BB564873	BB564873 BB564873
	15	70	19.0	252	14	BM783832	BM783832 K-EST0061
	16	57.6	15.6	272	10	BB574249	BB574249 BB574249
	17	57.2	15.5	358	10	BE486735	BE486735 174950 BA
	18	53.2	14.4	716	13	BI459541	BI459541 603200548
	19	52.8	14.3	464	9	AA667912	AA667912 vv19f07.r
	20	52.8	14.3	603	9	AI956381	AI956381 ul74e07.y
	21	52.8	14.3	674	10	BB613272	BB613272 BB613272
	22	52.8	14.3	754	11	AK008938	AK008938 Mus muscu
	23	51.8	14.0	311	10	AW869303	AW869303 MR3-SN006
c	24	51	13.8	424	13	BM389584	BM389584 UI-R-CN1-
c	25	51	13.8	760	14	BQ194830	BQ194830 UI-R-CN1-
	26	50.8	13.8	270	10	BB595946	BB595946 BB595946
	27	50.8	13.8	869	12	BF540248	BF540248 602050296
	28	45	12.2	986	17	CNS076KL	AL431515 T3 end of
	29	42.2	11.4	484	13	BJ059218	BJ059218 BJ059218
c	30	42.2	11.4	687	13	BJ098508	BJ098508 BJ098508
	31	42	11.4	597	13	BJ038615	BJ038615 BJ038615
	32	40.4	10.9	589	13	BJ094875	BJ094875 BJ094875
	33	40.4	10.9	629	13	BJ095114	BJ095114 BJ095114
	34	40.4	10.9	893	14	BQ734561	BQ734561 AGENCOURT
	35	39.8	10.8	309	13	BJ059046	BJ059046 BJ059046
c	36	38.4	10.4	634	10	AW187570	AW187570 BNLGH1777
	37	38.4	10.4	694	12	BF479357	BF479357 L48-3026T
	38	38.4	10.4	697	13	BM301804	BM301804 MCA045A01
	39	37.8	10.2	455	12	BG554741	BG554741 dac30h03.
	40	37.2	10.1	539	13	BI450048	BI450048 daa97c09.
c	41	36.6	9.9	375	14	BM971336	BM971336 UI-CF-EC1
c	42	36.6	9.9	591	14	BM984243	BM984243 UI-CF-EC1
	43	36.6	9.9	637	9	AL779553	AL779553 AL779553
	44	36.2	9.8	431	10	BB789522	BB789522 BB789522
c	45	36.2	9.8	772	10	BE273157	BE273157 601142325

ALIGNMENTS

RESULT 1
BG208163/c
LOCUS BG208163 803 bp mRNA linear EST 21-APR-2001
DEFINITION RST27654 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG208163
VERSION BG208163.1 GI:13729850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 550.
FEATURES Location/Qualifiers

```
     source          1. .803
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      222 a    172 c    171 g    238 t
ORIGIN

  Query Match             96.2%;  Score 354.8;  DB 12;  Length 803;
  Best Local Similarity   99.2%;  Pred. No. 3.3e-92;
  Matches  367;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG-AAGGATTTTTAT 59
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     688 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAAGGATTTTTAT 629

Qy      60 TACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAA 119
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 TACTTATATGTACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAA 569

Qy     120 AGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTT 179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 AGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTT 509

Qy     180 CTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTC 239
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     508 CTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCATGAGACGGGAACACTC 449

Qy     240 CAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAAT 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 CAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAAT 389

Qy     300 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 329

Qy     360 AATGTCCCCC 369
          ||||||||||
Db     328 AATGTCCCCC 319


RESULT 2
AI962650
LOCUS       AI962650                410 bp    mRNA    linear   EST 08-MAR-2000
DEFINITION  wq42e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473948 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI962650
VERSION     AI962650.1  GI:5755363
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 770    Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES            Location/Qualifiers
     source         1. .410
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2473948"
                    /clone_lib="NCI_CGAP_GC6"
                    /tissue_type="pooled germ cell tumors"
                    /lab_host="DH10B"
                    /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                    from the normalized library NCI_CGAP_GC4 was prepared, and
                    ss circles were made in vitro. Following HAP purification,
                    this DNA was used as tracer in a subtractive hybridization
                    reaction. The driver was PCR-amplified cDNAs from a pool
                    of 5,000 clones made from the same library (cloneIDs
                    1257096-1258631, 1469064-1470983, and 1475592-1476743).
                    Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      120 a     93 c     93 g    104 t
ORIGIN

  Query Match             90.2%;  Score 333;  DB 9;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-86;
  Matches  333;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 77

Qy      97 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 137

Qy     157 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 197

Qy     217 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 257

Qy     277 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     258 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 317

Qy     337 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 369
          |||||||||||||||||||||||||||||||||
Db     318 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 350


RESULT 3
AI654552
LOCUS       AI654552                429 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wb48b12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308895 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI654552
VERSION     AI654552.1  GI:4738531
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 771   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2308895"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      127 a    100 c     97 g    104 t      1 others
ORIGIN

  Query Match            90.2%;  Score 333;  DB 9;  Length 429;
  Best Local Similarity  100.0%;  Pred. No. 5.5e-86;
  Matches  333;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 71

Qy      97 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 131

Qy     157 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 191

Qy     217 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 251

Qy     277 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 311

Qy     337 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 369
           |||||||||||||||||||||||||||||||||
Db     312 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 344


RESULT 4
AI339609
LOCUS       AI339609                391 bp    mRNA    linear   EST 29-DEC-1998
DEFINITION  qq42a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935156
            3' similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI339609
VERSION     AI339609.1  GI:4076536
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1935156"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      119 a     93 c     93 g     86 t
ORIGIN

  Query Match            89.1%;  Score 328.8;  DB 9;  Length 391;
  Best Local Similarity  99.4%;  Pred. No. 8.8e-85;
  Matches  330;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      38 ACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTG 97
           |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       3 ACGTCTTCCGAAGGATTTTTATTACTTATGGGGACAATTGGCGCCAGAACACAACAGCTG 62

Qy      98 AGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACC 157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 AGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACC 122

Qy     158 TCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGA 217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 TCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGA 182

Qy     218 AATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGC 277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 AATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGC 242

Qy     278 AGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGA 337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 AGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGA 302

Qy     338 ACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 369
           |||||||||||||||||||||||||||||||
Db     303 ACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 334


RESULT 5
AI246239
LOCUS       AI246239                372 bp    mRNA    linear   EST 28-JAN-1999
DEFINITION  qi29g04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857942
            3' similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI246239
VERSION     AI246239.1  GI:3841636
```

```
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 921   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 365.
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1857942"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      115 a     89 c     86 g     82 t
ORIGIN

  Query Match             88.1%;  Score 325;  DB 9;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-83;
  Matches  325;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      45 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 60

Qy     105 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT 164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT 120

Qy     165 GATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 180

Qy     225 GAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAA 284
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAA 240

Qy     285 GTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGG 344
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGG 300

Qy     345 TGCGGCTGGGTTCAAAATGTCCCCC 369
           |||||||||||||||||||||||||
Db     301 TGCGGCTGGGTTCAAAATGTCCCCC 325


RESULT 6
AK008619
LOCUS       AK008619               1691 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male stomach cDNA, RIKEN full-length enriched
            library, clone:2200002I16:homolog to MINIMUM POTASSIUM ION
            CHANNEL-RELATED PEPTIDE 1 (MIRP1) (MINK-RELATED PEPTIDE 1), full
            insert sequence.
ACCESSION   AK008619
VERSION     AK008619.1  GI:12842913
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2200002I16.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1691)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
```

```
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
     source          1. .1691
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:2200002I16"
                     /db_xref="MGD:MGI:1901204"
                     /db_xref="taxon:10090"
                     /clone="2200002I16"
                     /sex="male"
                     /tissue_type="stomach"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             149. .520
                     /note="data source:SPTR, source key:Q9WTW0, evidence:ISS
                     homolog to MINIMUM POTASSIUM ION CHANNEL-RELATED PEPTIDE 1
                     (MIRP1) (MINK-RELATED PEPTIDE 1)
                     putative"
                     /codon_start=1
                     /protein_id="BAB25781.1"
                     /db_xref="GI:12842914"
                     /db_xref="MGD:MGI:1916393"
                     /translation="MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAE
                     NFYYVILYLMVMIGMFSFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQEKYKSQILH
                     LEDSKATIHENMGATGFTVSP"
     polyA_signal    1673. .1678
                     /note="putative"
     polyA_site      1691
                     /note="putative"
BASE COUNT      482 a    365 c    410 g    434 t
ORIGIN

  Query Match             72.2%;  Score 266.6;  DB 11;  Length 1691;
  Best Local Similarity   82.7%;  Pred. No. 1.8e-66;
  Matches  305;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||| | || ||| ||||||| || ||||| ||||| || | |||| || ||||||||||
Db     149 ATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAAAAAGATTTTTATT 208

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  ||| |   |||||| ||||| ||| |  |||| ||||| |||| |
Db     209 ACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGCACTCCAGGCCAGA 268

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           || ||||| |||||||||||||| ||||||||||||||||||||||||| || ||||||
Db     269 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 328

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           || |||||| | |||||||||||||||||||| ||||| || ||| | || || ||||||
Db     329 TCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGAGAGCACTCC 388

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           | ||||| |||||||||||||| || || || |||||||||||||||||| || || |||
Db     389 CAGGACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTACAAAAGTCAGATC 448

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           || |||| ||||| || |||||||||||||||||||||||| || ||| | |||||| |
Db     449 CTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACATGGGGGCGACGGGGTTCACA 508

Qy     361 ATGTCCCCC 369
           |||| |||
Db     509 GTGTCACCC 517


RESULT 7
D85797
LOCUS       D85797                   470 bp    mRNA    linear   EST 09-SEP-1996
DEFINITION  D85797 Rat 21 day old female ovary mRNA PMSG 3h Rattus norvegicus
            cDNA, mRNA sequence.
ACCESSION   D85797
VERSION     D85797.1  GI:1469812
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 470)
  AUTHORS   Miyamoto,K., Mizutani,T., Numata,Y. and Okada,T.
  TITLE     Rat 21 day old female ovary mRNA
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Miyamoto,K.
            Institute for Molecular and Cellular Reg
            Gunma Univ., Biosignal Research Center
            Shouwa machi 3-39-15, Maebashi, Gunma 371, Japan
            Email: tmizu@sb.gunma-u.ac.jp
            5'-59.
FEATURES             Location/Qualifiers
     source          1. .470
                     /organism="Rattus norvegicus"
                     /strain="Wistar"
                     /db_xref="taxon:10116"
                     /clone_lib="Rat 21 day old female ovary mRNA PMSG 3h"
                     /sex="female"
                     /tissue_type="ovary"
                     /dev_stage="21 day old"
                     /note="tissue_type=hypothalamus; dev_stage=adult rat"
BASE COUNT      116 a    127 c    128 g     95 t      4 others
ORIGIN

  Query Match             69.9%;  Score 257.8;  DB 14;  Length 470;
  Best Local Similarity   80.8%;  Pred. No. 4e-64;
  Matches  298;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||| | |||||| |||| || || ||||| ||||| || | |||| || | |||| |||
Db      37 ATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAAAAGGTTTTCATT 96

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  ||| |   |||||||||||| || ||| |||| ||||| |||| |
Db      97 ACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCGCTCCAGGCCAGA 156

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           || ||||| |||||||||||||| |||||||||||||||||||||||| || ||||||
Db     157 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 216

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           | |||||| | |||||||||||||||||||| ||||| || ||| | ||||| ||||||
Db     217 GCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGGGAGCACTCC 276
```

```
Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           | ||||| |||||||||| | | || ||||| |||||| | ||||| | ||| || |||
Db     277 CAGGACCCGTACCACCAGTNCNTCGTGGAGGATTGGCAGCAGAAGTATAGGAGTCAGATC 336

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           | | |||| ||||| || |||||||| ||||||||| ||| | || ||| | ||||||| |
Db     337 TNGCATCTGGAAGACTCCAAGGCCATCATCCATGATAACCTGGGGGCGACGGGGTTCACA 396

Qy     361 ATGTCCCCC 369
           |||| |||
Db     397 NTGTCACCC 405


RESULT 8
BG261965
LOCUS       BG261965               1003 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  602373784F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481325 5',
            mRNA sequence.
ACCESSION   BG261965
VERSION     BG261965.1  GI:12771781
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10316  row: g  column: 22
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .1003
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4481325"
                     /clone_lib="NIH_MGC_94"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      249 a    218 c    302 g    234 t
ORIGIN

  Query Match           65.6%;  Score 242;  DB 12;  Length 1003;
  Best Local Similarity   81.7%;  Pred. No. 2.1e-59;
  Matches  304;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    2;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||| | || ||| ||||||| || ||||| ||||| || | |||| || ||||||||||
Db      91 ATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAAAAAGATTTTTATT 150

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  ||| |   |||||| ||||| ||| |  |||| ||||| |||| |
Db     151 ACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGCACTCCAGGCCAGA 210

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           || ||||| |||||||||||||| ||||||||||||||||||||||||| || ||||||
Db     211 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 270

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           || |||||| | |||||||||||||||||||| ||||| || ||| | || || ||||||
Db     271 TCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGAGAGCACTCC 330

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           |  |||| |||||||||||||| || || || |||||||||||||||||| || || |||
Db     331 CAGCACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTACAAAAGTCAGATC 390

Qy     301 TTGAATCTAGAAGAATCGAA--GGCCACCATCCATGAGAACAT-TGGTGCGGCTGGGTTC 357
           || |||| ||||| || ||  ||||||||||||||||||||  || ||| | ||||||
Db     391 CTGCATCTGGAAGACTCCAAAGGGCCACCATCCATGAGAACATGGGGGGCGACGGGGTTC 450

Qy     358 AAAATGTCCCCC 369
           | | |||| |||
Db     451 ACAGTGTCACCC 462


RESULT 9
BG221966
LOCUS       BG221966               746 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST41783 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG221966
VERSION     BG221966.1  GI:13747987
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 547.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      241 a    138 c    123 g    243 t      1 others
ORIGIN

  Query Match           48.2%;  Score 177.8;  DB 12;  Length 746;
  Best Local Similarity   93.2%;  Pred. No. 8.4e-41;
  Matches  207;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     526 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 585

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           |||||||||||||||||||||||||||||| |||||||||| |||||||||| |||||||
Db     586 ACTTATATGGACAATTGGCGCCAGAACACACCAGCTGAGCAGGAGGCCCTCC-AGCCAAA 644

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
```

```
Db    645 GTTGATGCTGAGAACTTCTACTATGTCATCCCGGACCCAATGGNGATGATTGGAATGTTC 704

Qy    181 TCTTTCAT-CATCGTGGCCATCCTGGTGAGCACTGTGAAATC 221
Db    705 TTTTTAATAAATGGGGGCCATCCTGGGGAGCACTGTGAAATC 746


RESULT 10
BG938225
LOCUS       BG938225                351 bp    mRNA    linear   EST 11-JUN-2001
DEFINITION  1Abo14A12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
            sequence.
ACCESSION   BG938225
VERSION     BG938225.1  GI:14337597
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
  TITLE     cDNA's from bovine abomasum tissue
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dr. Stephen Moore
            . Beef Genomics Laboratory
            Dept of AFNS, University of Alberta
            410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
            Tel: 780 492 0169
            Fax: 780 492 4265
            Email: smoore@afns.ualberta.ca
            The sequence best matches gb:AP001719 (Homo sapiens genomic DNA,
            chromosome 21q, section 63/105) in main database at high score of
            212.0 and E-value of 9e-53
            PCR PRimers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Seq primer: T3 primer
            High quality sequence stop: 351
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="Bovine Abomasum cDNA Library"
                     /sex="Two males and one female mixed"
                     /tissue_type="Gastrointestinal tissue (GIT)"
                     /cell_type="Epithelial"
                     /dev_stage="Young adult"
                     /lab_host="XL1-BlueMRF'-strain"
                     /note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
                     I; Site_2: Xho I"
BASE COUNT      104 a     89 c     76 g     82 t
ORIGIN

  Query Match            45.6%;  Score 168.2;  DB 13;  Length 351;
  Best Local Similarity  87.1%;  Pred. No. 3.9e-38;
  Matches  196;  Conservative    0;  Mismatches   28;  Indels    1;  Gaps    1;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
Db    127 ATGCCAACTCTATCCAATCTGACACAGACACTGGAATATGTCTTCAAAAAGATTTTTATC 186

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
Db    187 ACTTACATGGAAAACTGGCACAGGAACACAACGGTTGAGCAAGAGGCCCTGCAAGCCAAG 246

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
Db    247 GTTGATGCTGAGAACTTCTACTATGTCATCTTGTACCTTATGGTGATGATCGGAATGTTC 306

Qy    181 TCTTT-CATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 224
Db    307 TCTTTCCATCATTGTAGCCATCCTGGTGAGCACGGTGAAATCCAA 351


RESULT 11
AA633404
LOCUS       AA633404                188 bp    mRNA    linear   EST 28-OCT-1997
DEFINITION  np69h11.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1131621 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AA633404
VERSION     AA633404.1  GI:2555264
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 188)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 785   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 167.
FEATURES             Location/Qualifiers
     source          1. .188
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1131621"
                     /clone_lib="NCI_CGAP_Br2"
                     /sex="female, pooled"
                     /tissue_type="breast"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from pooled bulk
                     breast tumor tissue, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  This library is the normalized version of
                     NCI_CGAP_Br1.1. Library was constructed by Bento Soares
                     and M. Fatima Bonaldo. "
BASE COUNT       66 a     45 c     45 g     32 t
ORIGIN

  Query Match            42.5%;  Score 157;  DB 9;  Length 188;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-35;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    213 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 272
Db      1 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 60

Qy    273 CTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCA 332
Db     61 CTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCA 120

Qy    333 TGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 369
Db    121 TGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCC 157
```

```
RESULT 12
AA935321
LOCUS       AA935321                121 bp    mRNA    linear   EST 07-JUL-1998
DEFINITION  oo71g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571680 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AA935321
VERSION     AA935321.1  GI:3092478
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 121)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 763   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .121
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1571680"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       33 a     31 c     28 g     29 t
ORIGIN

  Query Match             32.4%;  Score 119.4;  DB 9;  Length 121;
  Best Local Similarity   99.2%;  Pred. No. 3.8e-24;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     153 GTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCAC 212
           ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1 GTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCAACGTGGCCATCCTGGTGAGCAC 60

Qy     213 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 120

Qy     273 C 273
           |
Db     121 C 121


RESULT 13
AW869303/c
LOCUS       AW869303                311 bp    mRNA    linear   EST 22-MAY-2000
DEFINITION  MR3-SN0067-240400-006-f11 SN0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW869303
VERSION     AW869303.1  GI:8003356
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 311)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=MR3-SN0067-240
            400-006-f11&t3=2000-04-24&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 74.
FEATURES             Location/Qualifiers
     source          1. .311
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="SN0067"
                     /dev_stage="Adult"
                     /note="Organ: stomach_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       60 a     80 c     76 g     95 t
ORIGIN

  Query Match             26.8%;  Score 99;  DB 10;  Length 311;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-18;
  Matches  117;  Conservative    0;  Mismatches   10;  Indels    2;  Gaps    1;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATC 123

Qy      61 ACTTATATGGACAATTGG--CGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCA 118
           ||| |||||||||||| ||    | ||||||| |||||||||| ||||||||||||||||
Db     122 ACTCATATGGACAATCGGGCGCCGAGAACACGACAGCTGAGCGAGAGGCCCTCCAAGCCT 63

Qy     119 AAGTTGATG 127
           ||| |||||
Db      62 AAGATGATG 54


RESULT 14
BB564873
LOCUS       BB564873                314 bp    mRNA    linear   EST 29-NOV-2000
DEFINITION  BB564873 RIKEN full-length enriched, adult male stomach Mus
            musculus cDNA clone 2200002I16 5', mRNA sequence.
ACCESSION   BB564873
VERSION     BB564873.1  GI:11455765
```

```
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 314)
  AUTHORS   Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P.
            , Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
            ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
            Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
            Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A.,
            Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
            ,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .314
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="2200002I16"
                     /clone_lib="RIKEN full-length enriched, adult male
                     stomach"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
                     /lab_host="SOLR"
                     /note="Site_1: XhoI; Site_2: SstI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with XhoI and SstI."
BASE COUNT       98 a     77 c     74 g     65 t
ORIGIN

  Query Match             24.4%;  Score 90;  DB 10;  Length 314;
  Best Local Similarity   76.0%;  Pred. No. 1.9e-15;
  Matches  111;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
             ||| | || ||| ||||||| || || || ||||| || | ||||  ||  |||||||||
Db     149 ATGGCCACATTAGCCAATTTGACCCAAACACTGGAGGATGCCTTCAAAAAAATTTTTATT 208

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  |||     |||||||||| |  || |  |||| ||||||||||||
Db     209 ACTTATATGGACAGCTGGAAGAGGAACACAACATCCAAGGAGCAGGCACTCCAAGCCAAA 268

Qy     121 GTTGATGCTGAGAACTTCTACTATGT 146
           || || ||  |||| ||||||||| ||
Db     269 GTGGAAGCCAAGAATTTCTACTAGGT 294


RESULT 15
BM783832
LOCUS       BM783832                252 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0061845 S17N258215 Homo sapiens cDNA clone S17N258215-2-A12
            5', mRNA sequence.
ACCESSION   BM783832
VERSION     BM783832.1  GI:19132064
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2  row: A  column: 12
            High quality sequence stop: 252.
FEATURES             Location/Qualifiers
     source          1. .252
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S17N258215-2-A12"
                     /clone_lib="S17N258215"
                     /sex="M"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT       85 a     48 c     59 g     60 t
ORIGIN

  Query Match             19.0%;  Score 70;  DB 14;  Length 252;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-09;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     300 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      1 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 60

Qy    360 AATGTCCCCC 369
          ||||||||||
Db     61 AATGTCCCCC 70


Search completed: May 21, 2003, 21:37:55
Job time : 600.902 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 20:27:39 ; Search time 50.6076 Seconds
(without alignments)
9628.006 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_442
Perfect score: 369
Sequence: 1 atgtctactttatccaattt.....ctgggttcaaaatgtccccc 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	369	100.0	372	10	US-09-864-761-33139	Sequence 33139, A
	2	369	100.0	732	9	US-10-000-151B-5	Sequence 5, Appli
	3	369	100.0	113604	9	US-10-227-195A-1	Sequence 1, Appli
	4	369	100.0	113604	9	US-10-227-195A-2	Sequence 2, Appli
	5	312	84.6	312	10	US-09-864-761-20233	Sequence 20233, A
	6	295	79.9	450	10	US-09-864-761-3463	Sequence 3463, Ap
	7	233	63.1	471	10	US-09-864-761-16671	Sequence 16671, A
c	8	53.2	14.4	231	10	US-09-864-761-20783	Sequence 20783, A
c	9	53.2	14.4	390	10	US-09-864-761-17593	Sequence 17593, A
	10	53.2	14.4	1703	9	US-10-138-316-3	Sequence 3, Appli
c	11	53.2	14.4	113604	9	US-10-227-195A-1	Sequence 1, Appli
c	12	53.2	14.4	113604	9	US-10-227-195A-2	Sequence 2, Appli
c	13	50.8	13.8	468	10	US-09-864-761-4026	Sequence 4026, Ap
c	14	46	12.5	381	10	US-09-864-761-810	Sequence 810, App
	15	36	9.8	1146	10	US-09-853-386-111	Sequence 111, App
	16	36	9.8	1206	10	US-09-853-386-107	Sequence 107, App
	17	36	9.8	1206	10	US-09-853-386-117	Sequence 117, App
	18	36	9.8	1495	10	US-09-191-724-1	Sequence 1, Appli
	19	36	9.8	1582	10	US-09-191-724-14	Sequence 14, Appl
c	20	36	9.8	2579	10	US-09-822-830A-30	Sequence 30, Appl
	21	33.4	9.1	4104	9	US-09-992-598-277	Sequence 277, App
	22	33.4	9.1	4104	9	US-09-989-293A-277	Sequence 277, App
	23	33.4	9.1	4104	9	US-09-989-735-277	Sequence 277, App
	24	33.4	9.1	4104	9	US-09-990-444-277	Sequence 277, App
	25	33.4	9.1	4104	9	US-09-989-730-277	Sequence 277, App
	26	33.4	9.1	4104	9	US-09-990-436-277	Sequence 277, App
	27	33.4	9.1	4104	9	US-09-991-181-277	Sequence 277, App
	28	33.4	9.1	4104	9	US-09-993-687-277	Sequence 277, App
	29	33.4	9.1	4104	9	US-09-989-734-277	Sequence 277, App
	30	33.4	9.1	4104	9	US-10-028-072-449	Sequence 449, App
	31	33.4	9.1	4104	9	US-09-997-653-277	Sequence 277, App
	32	33.4	9.1	4104	9	US-09-993-667-277	Sequence 277, App
	33	33.4	9.1	4104	9	US-10-121-049-449	Sequence 449, App
	34	33.4	9.1	4104	9	US-10-123-904-449	Sequence 449, App
	35	33.4	9.1	4104	9	US-10-140-470-449	Sequence 449, App
	36	33.4	9.1	4104	9	US-09-990-438-277	Sequence 277, App
	37	33.4	9.1	4104	9	US-09-990-562-277	Sequence 277, App
	38	33.4	9.1	4104	9	US-09-997-428-277	Sequence 277, App
	39	33.4	9.1	4104	9	US-09-997-666-277	Sequence 277, App
	40	33.4	9.1	4104	9	US-10-175-746-449	Sequence 449, App
	41	33.4	9.1	4104	9	US-10-176-918-449	Sequence 449, App
	42	33.4	9.1	4104	9	US-10-176-921-449	Sequence 449, App
	43	33.4	9.1	4104	9	US-10-227-884-157	Sequence 157, App
	44	33.4	9.1	4104	9	US-09-990-711-277	Sequence 277, App
	45	33.4	9.1	4104	9	US-10-137-865-449	Sequence 449, App

ALIGNMENTS

RESULT 1
US-09-864-761-33139
; Sequence 33139, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

```
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33139
;   LENGTH: 372
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000120.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.67
;   OTHER INFORMATION: EST_HUMAN HIT: AI654552.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: Q9Y6J6, EVALUE 8.00e-67
;   OTHER INFORMATION: NT HIT: gi11526220, EVALUE 0.00e+00
US-09-864-761-33139

  Query Match             100.0%;  Score 369;  DB 10;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-115;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy     361 ATGTCCCCC 369
          |||||||||
Db     361 ATGTCCCCC 369


RESULT 2
US-10-000-151B-5
; Sequence 5, Application US/10000151B
; Publication No. US20030013136A1
; GENERAL INFORMATION:
;  APPLICANT: Balser, Jeffrey R.
;  APPLICANT:  George, Alfred L.
;  TITLE OF INVENTION: HUMAN KCR1 REGULATION OF HERG POTASSIUM CHANNEL BLOCK
;  FILE REFERENCE: Vanderbilt Ref No. US20030013136A1 VU0120; Attorney Docket No. US2003
;  CURRENT APPLICATION NUMBER: US/10/000,151B
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 732
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-000-151B-5

  Query Match             100.0%;  Score 369;  DB 9;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 2e-115;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442


RESULT 3
US-10-227-195A-1
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
;  APPLICANT: Cox, David
;  APPLICANT:  Arnold, Deana
;  TITLE OF INVENTION: Haplotype structure of chromosome 21
;  FILE REFERENCE: 1030U1
;  CURRENT APPLICATION NUMBER: US/10/227,195A
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 113604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7175, 7204, 36973, 66372, 76921, 81512, 88727
;   OTHER INFORMATION: n = G or C
US-10-227-195A-1

  Query Match             100.0%;  Score 369;  DB 9;  Length 113604;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-114;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17476 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 17535

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17536 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 17595

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17596 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 17655
```

```
Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17656 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 17715

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17716 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 17775

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17776 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 17835

Qy    361 ATGTCCCCC 369
          |||||||||
Db  17836 ATGTCCCCC 17844


RESULT 4
US-10-227-195A-2
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
;  APPLICANT: Cox, David
;  APPLICANT:  Arnold, Deana
;  TITLE OF INVENTION: Haplotype structure of chromosome 21
;  FILE REFERENCE: 1030U1
;  CURRENT APPLICATION NUMBER: US/10/227,195A
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 113604
;   TYPE: DNA
;   ORGANISM: Human
US-10-227-195A-2

  Query Match             100.0%;  Score 369;  DB 9;  Length 113604;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-114;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17476 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 17535

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17536 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 17595

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17596 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 17655

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17656 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 17715

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17716 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 17775

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17776 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 17835

Qy    361 ATGTCCCCC 369
          |||||||||
Db  17836 ATGTCCCCC 17844


RESULT 5
US-09-864-761-20233
; Sequence 20233, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20233
;   LENGTH: 312
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000052.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.88
;   OTHER INFORMATION: EST_HUMAN HIT: AI246239.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: Q9Y6J6, EVALUE 3.00e-55
;   OTHER INFORMATION: NT HIT: AF302095.1, EVALUE 0.00e+00
US-09-864-761-20233

  Query Match             84.6%;  Score 312;  DB 10;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-96;
  Matches  312;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy      54 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 60

Qy     114 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120

Qy     174 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 180

Qy     234 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 240

Qy     294 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 300

Qy     354 GTTCAAAATGTC 365
           ||||||||||||
Db     301 GTTCAAAATGTC 312


RESULT 6
US-09-864-761-3463
; Sequence 3463, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3463
;   LENGTH: 450
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000052.1
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.92
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.88
US-09-864-761-3463

  Query Match             79.9%;  Score 295;  DB 10;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-90;
  Matches  295;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 215

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 275

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 335

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 395

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCC 295
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCC 450


RESULT 7
US-09-864-761-16671
; Sequence 16671, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
```

```
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16671
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000120.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.67
US-09-864-761-16671

  Query Match             63.1%;  Score 233;  DB 10;  Length 471;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-69;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 298

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 358

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 418

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 233
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 471


RESULT 8
US-09-864-761-20783/c
; Sequence 20783, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20783
;   LENGTH: 231
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000121.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
;   OTHER INFORMATION: SWISSPROT HIT: P15382, EVALUE 2.00e-39
;   OTHER INFORMATION: EST_HUMAN HIT: AW847275.1, EVALUE 5.60e-01
;   OTHER INFORMATION: NT HIT: AF135188.1, EVALUE 1.00e-127
US-09-864-761-20783

  Query Match             14.4%;  Score 53.2;  DB 10;  Length 231;
  Best Local Similarity   63.6%;  Pred. No. 5.6e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    207 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 148

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    147 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 88

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          || | |||||| || ||| |||||  | |  ||
Db     87 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 54


RESULT 9
```

```
US-09-864-761-17593/c
; Sequence 17593, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17593
;   LENGTH: 390
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000168.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
;   OTHER INFORMATION: EST_HUMAN HIT: AA770188.1, EVALUE 6.30e-02
;   OTHER INFORMATION: SWISSPROT HIT: P15382, EVALUE 4.00e-61
;   OTHER INFORMATION: NT HIT: gi11526222, EVALUE 0.00e+00
US-09-864-761-17593

  Query Match           14.4%;  Score 53.2;  DB 10;  Length 390;
  Best Local Similarity   63.6%;  Pred. No. 7.5e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     209 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 150

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     149 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 90

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | ||||||  || ||| |||||  | |  ||
Db      89 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 56


RESULT 10
US-10-138-316-3
; Sequence 3, Application US/10138316
; Publication No. US20030054380A1
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-162
;  CURRENT APPLICATION NUMBER: US/10/138,316
;  CURRENT FILING DATE:  2002-05-06
;  PRIOR APPLICATION NUMBER: 09/444,295
;  PRIOR FILING DATE: 1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
;   FEATURE:
;   NAME/KEY: misc
;   LOCATION: (1)..(1703)
;   OTHER INFORMATION: n may be any nucleotide
US-10-138-316-3

  Query Match           14.4%;  Score 53.2;  DB 9;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 1.8e-07;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | ||||||  || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477
```

```
RESULT 11
US-10-227-195A-1/c
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
;  APPLICANT: Cox, David
;  APPLICANT:  Arnold, Deana
;  TITLE OF INVENTION: Haplotype structure of chromosome 21
;  FILE REFERENCE: 1030U1
;  CURRENT APPLICATION NUMBER: US/10/227,195A
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 113604
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 7175, 7204, 36973, 66372, 76921, 81512, 88727
;   OTHER INFORMATION: n = G or C
US-10-227-195A-1

  Query Match             14.4%;  Score 53.2;  DB 9;  Length 113604;
  Best Local Similarity   63.6%;  Pred. No. 2e-06;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db   96499 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 96440

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db   96439 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 96380

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db   96379 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 96346


RESULT 12
US-10-227-195A-2/c
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
;  APPLICANT: Cox, David
;  APPLICANT:  Arnold, Deana
;  TITLE OF INVENTION: Haplotype structure of chromosome 21
;  FILE REFERENCE: 1030U1
;  CURRENT APPLICATION NUMBER: US/10/227,195A
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 113604
;   TYPE: DNA
;   ORGANISM: Human
US-10-227-195A-2

  Query Match             14.4%;  Score 53.2;  DB 9;  Length 113604;
  Best Local Similarity   63.6%;  Pred. No. 2e-06;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db   96499 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 96440

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db   96439 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 96380

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db   96379 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 96346


RESULT 13
US-09-864-761-4026/c
; Sequence 4026, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4026
;   LENGTH: 468
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000121.1
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.94
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
US-09-864-761-4026

  Query Match             13.8%;  Score 50.8;  DB 10;  Length 468;
  Best Local Similarity   63.3%;  Pred. No. 5.5e-07;
```

```
  Matches   95;  Conservative    0;  Mismatches   52;  Indels    3;  Gaps    1;

Qy     154 TACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACT 213
           ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || |||||
Db     467 TACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAGCTAC 408

Qy     214 GTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---TAGAG 270
           |    |||||||  | ||| |||||| || ||||| | | ||   |||||  |     ||
Db     407 ATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTCCGAT 348

Qy     271 GACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           | |||||| || ||| |||||  | |  ||
Db     347 GCCTGGCAAGAGAAGGACAAGGCCTATGTC 318


RESULT 14
US-09-864-761-810/c
; Sequence 810, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 810
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000168.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
US-09-864-761-810

  Query Match             12.5%;  Score 46;  DB 10;  Length 381;
  Best Local Similarity   64.2%;  Pred. No. 2.1e-05;
  Matches   86;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    1;

Qy     170 TTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGAC 229
           | ||| | |||   ||| ||| | ||| |||| || |||||    |    ||||||| |
Db     378 TGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAGCTACATCCGCTCCAAGAAGC 319

Qy     230 GGGAACACTCCAATGACCCCTACCACCAGTACATTGTA---GAGGACTGGCAGGAAAAGT 286
           ||| ||||| || ||||| | | ||   ||||| |     || | |||||| || |||
Db     318 TGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTCCGATGCCTGGCAAGAGAAGG 259

Qy     287 ACAAGAGCCAAATC 300
           |||||  | |  ||
Db     258 ACAAGGCCTATGTC 245


RESULT 15
US-09-853-386-111
; Sequence 111, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Evelyn
;  APPLICANT:  Bresnihan, Barry
;  APPLICANT:  Conneely, Orla
;  APPLICANT:  Fitzgerald, Oliver
;  TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
;  TITLE OF INVENTION:  Subfamily of Nuclear Transcription Factors
;  FILE REFERENCE: P01972US1
;  CURRENT APPLICATION NUMBER: US/09/853,386
;  CURRENT FILING DATE:  2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/203645
;  PRIOR FILING DATE: 2000-05-12
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
;   LENGTH: 1146
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-853-386-111

  Query Match              9.8%;  Score 36;  DB 10;  Length 1146;
  Best Local Similarity   52.7%;  Pred. No. 0.1;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     679 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 738

Qy     175 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 234
           || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db     739 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 798

Qy     235 CACTCCAATGACCCCTACCACCAGTACA 262
           | |||          |   |||||||
Db     799 TCCACCACGTCTGAGACCATTCAGTACA 826


Search completed: May 21, 2003, 22:43:31
Job time : 138.608 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 19:16:44 ; Search time 89.8202 Seconds
(without alignments)
9251.680 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_442
Perfect score: 369
Sequence: 1 atgtctactttatccaatttt.....ctgggttcaaaatgtccccc 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	369	100.0	372	22	AAI24432	Probe #14365 for g
2	369	100.0	372	22	AAI09965	Probe #9956 used t
3	369	100.0	372	22	AAS00245	Human potassium ch
4	369	100.0	471	22	AAF80269	Nucleotide sequenc
5	369	100.0	600	22	ABA09192	Human MiRP1 homolo
6	369	100.0	600	22	AAK52645	Human polynucleoti
7	369	100.0	655	22	AAK51661	Human polynucleoti
8	369	100.0	732	21	AAC64071	Human potassium ch
9	369	100.0	732	24	ABK86573	cDNA encoding huma
10	369	100.0	732	24	AAD35170	Human KCNE2 wild t
11	367.4	99.6	732	21	AAC64083	Human potassium ch
12	367.4	99.6	732	21	AAC64084	Human potassium ch
13	367.4	99.6	732	21	AAC64085	Human potassium ch
14	367.4	99.6	732	21	AAC64086	Human potassium ch
15	367.4	99.6	732	24	AAD35169	Human KCNE2 mutant
16	367.4	99.6	732	24	AAD35171	Human KCNE2 mutant
17	367.4	99.6	732	24	AAD35172	Human KCNE2 mutant
18	367.4	99.6	732	24	AAD35173	Human KCNE2 mutant
19	312	84.6	312	22	ABA49938	Human breast cell
20	312	84.6	312	22	ABA67856	Human foetal liver
21	312	84.6	312	22	ABA34913	Probe #13379 for g
22	312	84.6	312	22	AAK16264	Human brain expres
23	312	84.6	312	22	AAK42008	Human bone marrow
24	312	84.6	312	22	AAI22773	Probe #12706 for g
25	312	84.6	312	22	AAI48075	Probe #16761 used
26	312	84.6	312	22	AAI08446	Probe #8437 used t
27	312	84.6	312	24	ABS16039	Human genome-deriv
28	295	79.9	450	22	ABA44797	Human breast cell
29	295	79.9	450	22	ABA55252	Human foetal liver
30	295	79.9	450	22	ABA24997	Probe #3463 for ge
31	295	79.9	450	22	AAK03508	Human brain expres
32	295	79.9	450	22	AAK28962	Human bone marrow
33	295	79.9	450	22	AAI13549	Probe #3482 for ge
34	295	79.9	450	22	AAI34911	Probe #3597 used t
35	295	79.9	450	22	AAI03438	Probe #3429 used t
36	295	79.9	450	24	ABS03496	Human genome-deriv
37	263.4	71.4	372	22	AAS00246	Rat potassium chan
38	263.4	71.4	468	21	AAC64072	Rat potassium chan
39	233	63.1	471	22	AAI15256	Probe #5189 for ge
40	233	63.1	471	22	AAI04990	Probe #4981 used t
41	53.8	14.6	65	24	ABN29241	Rat spliced transc
c 42	53.2	14.4	231	22	ABA68478	Human foetal liver
c 43	53.2	14.4	231	22	ABA35463	Probe #13929 for g
c 44	53.2	14.4	231	22	AAK16847	Human brain expres
c 45	53.2	14.4	231	22	AAI23369	Probe #13302 for g

ALIGNMENTS

RESULT 1
AAI24432
ID AAI24432 standard; DNA; 372 BP.
XX
AC AAI24432;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #14365 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

```
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 14365; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;

  Query Match             100.0%;  Score 369;  DB 22;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy    361 ATGTCCCCC 369
          |||||||||
Db    361 ATGTCCCCC 369


RESULT 2
AAI09965
ID   AAI09965 standard; DNA; 372 BP.
XX
AC   AAI09965;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Probe #9956 used to measure gene expression in human breast sample.
XX
KW   Probe; human; breast disease; breast cancer; development disorder; ss;
KW   inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS   Homo sapiens.
XX
PN   WO200157270-A2.
XX
PD   09-AUG-2001.
XX
PF   29-JAN-2001; 2001WO-US00661.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-476286/51.
XX
PT   Novel single exon nucleic acid probe used to measuring gene expression
PT   in a human breast -
XX
PS   Claim 25; SEQ ID No 9956; 322pp; English.
XX
CC   The present invention relates to novel single exon nucleic acid probes.
CC   The present sequence is one such probe. The probes are useful for
CC   measuring human gene expression in a human breast sample, where the probe
CC   hybridises at high stringency to a nucleic acid expressed in the human
CC   breast. The probes are useful for predicting, diagnosing, grading,
CC   staging, monitoring and prognosing diseases of the human breast,
CC   particularly those diseases with polygenic aetiology. The diseases
CC   include: breast cancer, disorders of development, inflammatory diseases
CC   of the breast, fibrocystic changes, proliferative breast disease and
CC   non-carcinoma tumours.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;

  Query Match             100.0%;  Score 369;  DB 22;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy    361 ATGTCCCCC 369
          |||||||||
Db    361 ATGTCCCCC 369


RESULT 3
AAS00245
ID   AAS00245 standard; DNA; 372 BP.
```

```
XX
AC   AAS00245;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Human potassium channel regulatory protein, Mink2, DNA sequence.
XX
KW   Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
KW   angina; asthma; diabetes; renal insufficiency; urinary incontinence;
KW   irritable colon; epilepsy; cerebrovascular ischaemia; autoimmune disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..372
FT                   /*tag= a
FT                   /product= "MINK2 potassium channel protein"
XX
PN   WO200114403-A1.
XX
PD   01-MAR-2001.
XX
PF   18-AUG-2000; 2000WO-US22799.
XX
PR   20-AUG-1999;   99US-0379201.
XX
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   Ficker E,  Wible B,  Brown AM;
XX
DR   WPI; 2001-218424/22.
DR   P-PSDB; AAU00215.
XX
PT   Novel potassium channel gene termed MinK2 encoding potassium channel
PT   regulatory protein, useful for screening compounds that are useful for
PT   treating diseases caused by aberrant potassium activity -
XX
PS   Claim 1; Fig 9; 39pp; English.
XX
CC   The sequence represents the coding sequence of human potassium channel
CC   regulatory protein, Mink2. Mink2 sequence is useful for producing a
CC   potassium channel regulatory protein useful for in vitro or in vivo
CC   screening of agonistic or antagonistic compounds that are useful for
CC   treating diseases caused by aberrant potassium activity, such as human
CC   cardiac arrhythmias, hypertension, angina, asthma, diabetes, renal
CC   insufficiency, urinary incontinence, irritable colon, epilepsy,
CC   cerebrovascular ischaemia, and autoimmune disease.
XX
SQ   Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;

  Query Match             100.0%;  Score 369;  DB 22;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy    361 ATGTCCCCC 369
          |||||||||
Db    361 ATGTCCCCC 369


RESULT 4
AAF80269
ID   AAF80269 standard; DNA; 471 BP.
XX
AC   AAF80269;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Nucleotide sequence of human potassium channel subunit IsK2.
XX
KW   Human; potassium channel; IsK2; gene therapy; gastric motility;
KW   gastric acid secretion; anti-arrhythmic agent; myocardial infarction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             79..450
FT                   /*tag= a
FT                   /product= "potassium channel subunit IsK2"
XX
PN   WO200127246-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-US28014.
XX
PR   12-OCT-1999;   99US-0158781.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Swanson RJ,  Liu Y,  Folander K;
XX
DR   WPI; 2001-273764/28.
DR   P-PSDB; AAB67800.
XX
PT   New DNA encoding the IsK2 potassium channel subunit, useful e.g. for
PT   detecting mutations and screening for therapeutic agents  -
XX
PS   Claim 3; Fig 1A; 46pp; English.
XX
CC   The present sequence encodes a human potassium channel subunit,
CC   designated IsK2. The IsK2 polynucleotide, and derived probes, are
CC   used diagnostically to detect mutations in the IsK2 gene, to determine
CC   levels of mRNA expression and to isolate homologous sequences; for
CC   recombinant expression of IsK2; in gene therapy to increase potassium
CC   channel activity and to generate transgenic animals, as models and
CC   for drug screening. Recombinant IsK2 is used for studying biochemical
CC   activity of IsK2 and its role in disorders of gastric motility and
CC   gastric acid secretion, and to raise specific antibodies. IsK2
CC   modulators are potentially useful for treating diseases associated with
CC   increased or reduced potassium channel activity, e.g. as
CC   anti-arrhythmic agents for treating myocardial infarction and as
CC   regulators of gastric acid secretion.
XX
SQ   Sequence 471 BP; 143 A; 110 C; 103 G; 115 T; 0 other;

  Query Match             100.0%;  Score 369;  DB 22;  Length 471;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     79 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 138
```

```
Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 198

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     199 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 258

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     259 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 318

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 378

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     379 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 438

Qy     361 ATGTCCCCC 369
           |||||||||
Db     439 ATGTCCCCC 447
```

RESULT 5
ABA09192
ID ABA09192 standard; cDNA; 600 BP.
XX
AC ABA09192;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human MiRP1 homologue-encoding cDNA, SEQ ID NO:968.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11948.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 826; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other;

```
  Query Match             100.0%;  Score 369;  DB 22;  Length 600;
  Best Local Similarity   100.0%;  Pred. No. 3e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 97

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 157

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 217

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 277

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 337

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 397

Qy     361 ATGTCCCCC 369
           |||||||||
Db     398 ATGTCCCCC 406
```

```
RESULT 6
AAK52645
ID   AAK52645 standard; cDNA; 600 BP.
XX
AC   AAK52645;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 2174.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79512.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 4539-4540; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other;

  Query Match           100.0%;  Score 369;  DB 22;  Length 600;
  Best Local Similarity  100.0%;  Pred. No. 3e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 97

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 157

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 217

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 277

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 337

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 397

Qy    361 ATGTCCCCC 369
          |||||||||
Db    398 ATGTCCCCC 406


RESULT 7
AAK51661
ID   AAK51661 standard; cDNA; 655 BP.
XX
AC   AAK51661;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 206.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM78528.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 1024; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
```

```
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 655 BP; 196 A; 154 C; 146 G; 153 T; 6 other;

  Query Match            100.0%;  Score 369;  DB 22;  Length 655;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      93 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 152

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     153 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 212

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     213 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 272

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     273 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 332

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     333 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 392

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     393 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 452

Qy     361 ATGTCCCCC 369
          |||||||||
Db     453 ATGTCCCCC 461


RESULT 8
AAC64071
ID   AAC64071 standard; cDNA; 732 BP.
XX
AC   AAC64071;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) cDNA, SEQ ID NO:1.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29585.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 1; Page 118-119; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents cDNA encoding human KCNE2 (MiRP1).
XX
SQ   Sequence 732 BP; 221 A; 152 C; 157 G; 202 T; 0 other;

  Query Match            100.0%;  Score 369;  DB 21;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442


RESULT 9
ABK86573
ID   ABK86573 standard; DNA; 732 BP.
```

```
XX
AC   ABK86573;
XX
DT   24-SEP-2002  (first entry)
XX
DE   cDNA encoding human ether-a-go-go related interacting protein MiRP1.
XX
KW   Human; human ether-a-go-go related gene; HERG; KCR1; MiRP1;
KW   long QT syndrome; LQT; single nucleotide polymorphism; cardiac arrythmia;
KW   potassium channel; ss; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "MiRP1"
XX
PN   WO200242735-A2.
XX
PD   30-MAY-2002.
XX
PF   30-OCT-2001; 2001WO-US45644.
XX
PR   30-OCT-2000; 2000US-244340P.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   Balser JR,  George AL,  Roden DM;
XX
DR   WPI; 2002-527650/56.
DR   P-PSDB; AAU99168.
XX
PT   Identifying a potassium channel activity modulator for drug design,
PT   comprises contacting a compound with a potassium channel and rat
PT   cerebellar cDNA library (KCR1) polypeptide, and determining activity -
XX
PS   Claim 17; Page 162-163; 164pp; English.
XX
CC   The invention relates to identifying (M1) a compound that modulates
CC   biological activity of a potassium channel (PC), by contacting a
CC   compound with a structure comprising a PC polypeptide and a polypeptide
CC   cloned from a rat cerebellar cDNA library (KCR1), and determining the
CC   activity of the PC polypeptide in the presence and absence of the
CC   compound, where a difference in the activities indicates modulation of
CC   biological activity of PC. Also include are identifying (M2) a candidate
CC   compound that modulates the biological activity of a complex comprising a
CC   human ether-a-go-go-related gene (HERG) channel polypeptide and a KCR1
CC   polypeptide, identifying (M3) a candidate compound as a modulator of KCR1
CC   expression, modulating (M4) PC function in a subject, comprising
CC   administering to the subject a substance that provides expression of a
CC   KCR1-encoding nucleic acid molecule in a cell or tissue, where modulated
CC   PC function is desired, screening (M5) for susceptibility to a drug-
CC   induced cardiac arrhythmia in a subject, comprising obtaining a
CC   biological sample from the subject and detecting a polymorphism of a KCR1
CC   gene in the biological sample from the subject, where the presence of the
CC   polymorphism indicates the susceptibility of the subject to a
CC   drug-induced cardiac arrhythmia, an oligonucleotide pair, where a first
CC   oligonucleotide of the pair hybridises to a first portion of a KCR1 gene
CC   which includes a polymorphism of the KCR1 gene, and the second
CC   oligonucleotide of the pair hybridises to a second portion of the KCR1
CC   gene that is adjacent to the first portion and a set of antisense
CC   oligonucleotide primers, suitable for amplifying a portion of a KCR1 gene
CC   which includes a polymorphism of the KCR1 gene. (M1) is useful for
CC   identifying a compound that modulates biological activity of PC,
CC   especially HERG, for modulating PC function (i.e modulating HERG
CC   activity) in a mammal, by preparing a composition comprising the
CC   compound and administering the composition. The compound is useful for
CC   treating or preventing long QT syndrome (LOT) and is useful in drug
CC   designing. The present sequence encodes a HERG interacting
CC   protein MiRP1 (not defined).
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
```

```
  Query Match           100.0%;  Score 369;  DB 24;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442
```

```
RESULT 10
AAD35170
ID   AAD35170 standard; DNA; 732 BP.
XX
AC   AAD35170;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human KCNE2 wild type DNA.
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "Human MiRP1 protein"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   P-PSDB; AAE22095.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
```

```
PS   Claim 9; Page 43; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human KCNE2 wild type DNA.
XX
SQ   Sequence 732 BP; 221 A; 152 C; 157 G; 202 T; 0 other;

  Query Match             100.0%;  Score 369;  DB 24;  Length 732;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442


RESULT 11
AAC64083
ID   AAC64083 standard; DNA; 732 BP.
XX
AC   AAC64083;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) Q9E mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29593.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 151 C; 158 G; 202 T; 0 other;

  Query Match             99.6%;  Score 367.4;  DB 21;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 9.9e-101;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACAGAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
```

```
          |||||||||
Db    434 ATGTCCCCC 442


RESULT 12
AAC64084
ID   AAC64084 standard; DNA; 732 BP.
XX
AC   AAC64084;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) M54T mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29594.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

  Query Match           99.6%;  Score 367.4;  DB 21;  Length 732;
  Best Local Similarity  99.7%;  Pred. No. 9.9e-101;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCACGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442


RESULT 13
AAC64085
ID   AAC64085 standard; DNA; 732 BP.
XX
AC   AAC64085;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) I57T mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29595.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
```

```
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

  Query Match             99.6%;  Score 367.4;  DB 21;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 9.9e-101;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGACTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
           |||||||||
Db     434 ATGTCCCCC 442


RESULT 14
AAC64086
ID   AAC64086 standard; DNA; 732 BP.
XX
AC   AAC64086;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) T8A mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29596.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 220 A; 152 C; 158 G; 202 T; 0 other;

  Query Match             99.6%;  Score 367.4;  DB 21;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 9.9e-101;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCGCACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253
```

```
Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCC 369
          |||||||||
Db    434 ATGTCCCCC 442


RESULT 15
AAD35169
ID   AAD35169 standard; DNA; 732 BP.
XX
AC   AAD35169;
XX
DT   25-JUL-2002  (first entry)
XX
DE   Human KCNE2 mutant DNA (C420T).
XX
KW   Human; Min-K related ion channel protein; MiRP1; ion channel disorder;
KW   KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; mutant; gene; SNP;
KW   single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             74..445
FT                   /*tag= a
FT                   /product= "Human MiRP1 mutant protein"
FT   variation       replace (420, C)
FT                   /*tag= b
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200222875-A2.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US28332.
XX
PR   11-SEP-2000; 2000US-231571P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goldstein SAN;
XX
DR   WPI; 2002-362360/39.
DR   P-PSDB; AAE22094.
XX
PT   Novel gene encoding Min-K related ion channel protein subunit and
PT   polymorphisms in this gene associated with antibiotic-induced long QT
PT   syndrome -
XX
PS   Claim 1; Page 41-42; 49pp; English.
XX
CC   The present invention relates to novel KCNE2 genes encoding Min-K related
CC   (MiRP) 1 ion channel proteins and polymorphisms in these genes that are
CC   associated with ion channel disorders including antibiotic-induced long
CC   QT syndrome (LQTS). Detecting a mutation at amino acid positions 8, 54,
CC   57 or 116 of MiRP1 polypeptide or a mutation at a nucleotide position
CC   encoding the amino acid positions is useful for diagnosing the presence
CC   of a polymorphism that causes drug-induced LQTS. The diagnostic methods
CC   are useful in the development of new drug therapies which selectively
CC   target one or more KCNE2 polymorphisms that are associated with cardiac
CC   arrhythmias. The present sequence is human KCNE2 mutant DNA (C420T).
XX
SQ   Sequence 732 BP; 221 A; 151 C; 157 G; 203 T; 0 other;

  Query Match            99.6%;  Score 367.4;  DB 24;  Length 732;
  Best Local Similarity  99.7%;  Pred. No. 9.9e-101;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGTGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCC 369
          |||||||||
Db    434 ATGTCCCCC 442


Search completed: May 21, 2003, 20:27:32
Job time : 95.8202 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 19:44:14 ; Search time 803.354 Seconds
(without alignments)
13367.622 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_442
Perfect score: 369
Sequence: 1 atgtctactttatccaatttt.....ctgggttcaaaatgtccccc 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		369	100.0	732	6	AX406941	AX406941 Sequence
2		369	100.0	732	9	AF071002	AF071002 Homo sapi
3		369	100.0	809	9	AF302095	AF302095 Homo sapi
4		369	100.0	24608	9	AP000320	AP000320 Homo sapi
5		369	100.0	100000	9	AP000052	AP000052 Homo sapi
6		369	100.0	100000	9	AP000167	AP000167 Homo sapi
7		369	100.0	100000	17	AP000120	Ap000120 Homo sapi
8		369	100.0	340000	9	AP001719	AP001719 Homo sapi
9		367.4	99.6	732	6	AX406939	AX406939 Sequence
10		367.4	99.6	732	6	AX406943	AX406943 Sequence
11		367.4	99.6	732	6	AX406945	AX406945 Sequence
12		367.4	99.6	732	6	AX406947	AX406947 Sequence
13		265	71.8	1664	10	BC022699	BC022699 Mus muscu
14		263.4	71.4	372	10	AY050513	AY050513 Cavia por
15		263.4	71.4	468	10	AF071003	AF071003 Rattus no
16	c	261.8	70.9	144709	2	AC117904	AC117904 Rattus no
17		186.6	50.6	225	4	AY079211	AY079211 Sus scrof
18		186.2	50.5	215	4	AF329636	AF329636 Oryctolag
19		178.2	48.3	228	4	AF387764	AF387764 Equus cab
20		56	15.2	534	4	RABIPCS	L41659 Oryctolagus
21		55	14.9	750	10	GPIISK	L20462 Cavia cobay
22		53.2	14.4	390	9	AF135188	AF135188 Homo sapi
23		53.2	14.4	390	10	AY050512	AY050512 Cavia por
24		53.2	14.4	398	6	I40373	I40373 Sequence 5
25		53.2	14.4	402	9	HUMISKA	L33815 Homo sapien
26		53.2	14.4	408	9	HUMCDRPCA	L28168 Homo sapien
27		53.2	14.4	436	9	HUMISK	M26685 Human IsK p
28		53.2	14.4	1703	6	AR119312	AR119312 Sequence
29		53.2	14.4	1703	6	AR164693	AR164693 Sequence
30		53.2	14.4	3173	9	BC036452	BC036452 Homo sapi
31	c	53.2	14.4	43126	9	AP000324	AP000324 Homo sapi
32	c	53.2	14.4	100000	9	AP000053	AP000053 Homo sapi
33	c	53.2	14.4	100000	9	AP000168	AP000168 Homo sapi
34	c	53.2	14.4	100000	17	AP000121	Ap000121 Homo sapi
35	c	53.2	14.4	340000	9	AP001720	AP001720 Homo sapi
36		52.8	14.3	611	10	MMKCHA	X60457 M.musculus
37		52.6	14.3	393	4	AB032575	AB032575 Sus scrof
38		51	13.8	471	10	RATDRTKCA	M36461 Rat delayed
39		51	13.8	585	10	RATPCPA	M22412 Rat potassi
40		50.8	13.8	153306	2	AL807829	AL807829 Danio rer
41		50.4	13.7	390	4	MSU62404	U62404 Felis catus
42		44.6	12.1	422	12	SYNMINK	M64922 Synthetic v
43	c	41	11.1	6408	6	AX346023	AX346023 Sequence
44	c	39	10.6	161482	2	AP004643	AP004643 Oryza sat
45		38.6	10.5	4881	3	DSPTEH2	X60437 Drosophila

ALIGNMENTS

RESULT 1
AX406941
LOCUS AX406941 732 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 3 from Patent WO0222875.
ACCESSION AX406941
VERSION AX406941.1 GI:21439816
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Goldstein,S.A.
TITLE Polymorphisms associated with cardiac arrythmia
JOURNAL Patent: WO 0222875-A 3 21-MAR-2002;

```
          YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, wild type"
                     /codon_start=1
                     /protein_id="CAD35180.1"
                     /db_xref="GI:21439817"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      221 a    152 c    157 g    202 t
ORIGIN

  Query Match           100.0%;  Score 369;  DB 6;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442


RESULT 2
AF071002
LOCUS       AF071002                732 bp    mRNA    linear   PRI 29-APR-1999
DEFINITION  Homo sapiens minK-related peptide 1 mRNA, complete cds.
ACCESSION   AF071002
VERSION     AF071002.1  GI:4704422
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 732)
  AUTHORS   Abbott,G.W., Sesti,F., Splawski,I., Buck,M.E., Lehmann,M.H.,
            Timothy,K.W., Keating,M.T. and Goldstein,S.A.
  TITLE     MiRP1 forms IKr potassium channels with HERG and is associated with
            cardiac arrhythmia
  JOURNAL   Cell 97 (2), 175-187 (1999)
  MEDLINE   99235979
   PUBMED   10219239
REFERENCE   2  (bases 1 to 732)
  AUTHORS   Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Section of Developmental Biology and
            Biophysics, Department of Pediatrics and Boyer Center for Molecular
            Medicine, Yale University School of Medicine, 295 Congress Avenue,
            New Haven, CT 06536, USA
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q11.1"
                     /tissue_type="heart"
     CDS             74. .445
                     /note="potassium channel subunit; MiRP1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAD28086.1"
                     /db_xref="GI:4704423"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      221 a    152 c    157 g    202 t
ORIGIN

  Query Match           100.0%;  Score 369;  DB 9;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 8.6e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
          |||||||||
Db     434 ATGTCCCCC 442


RESULT 3
AF302095
LOCUS       AF302095                809 bp    mRNA    linear   PRI 14-SEP-2000
DEFINITION  Homo sapiens voltage-gated K+ channel subunit MIRP1 (KCNE2) mRNA,
            complete cds.
ACCESSION   AF302095
VERSION     AF302095.1  GI:10121887
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 809)
  AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
  TITLE     Cloning of human MIRP1 cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 809)
  AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
  TITLE     Direct Submission
```

```
  JOURNAL   Submitted (01-SEP-2000) Medical and Molecular Genetics Center,
            Institut Recerca Oncologica, Avia. de Castelldefels Km 2,7,
            L'Hospitalet de Llobregat, Barcelona 08907, Spain
FEATURES             Location/Qualifiers
     source          1. .809
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22"
     gene            1. .809
                     /gene="KCNE2"
     CDS             141. .512
                     /gene="KCNE2"
                     /codon_start=1
                     /product="voltage-gated K+ channel subunit MIRP1"
                     /protein_id="AAG13416.1"
                     /db_xref="GI:10121888"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      247 a    172 c    189 g    200 t      1 others
ORIGIN

  Query Match            100.0%;  Score 369;  DB 9;  Length 809;
  Best Local Similarity  100.0%;  Pred. No. 8.8e-101;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 200

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 260

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 320

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 380

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 440

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     441 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 500

Qy     361 ATGTCCCCC 369
          |||||||||
Db     501 ATGTCCCCC 509


RESULT 4
AP000320
LOCUS       AP000320               24608 bp    DNA     linear   PRI 20-NOV-1999
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
            clone:Q12C8, complete sequence.
ACCESSION   AP000320
VERSION     AP000320.1  GI:4835689
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:Q12C8.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24608)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Homo sapiens 24,608bp genomic DNA of 21q22.1
  JOURNAL   Published Only in DataBase (1999)

REFERENCE   2  (bases 1 to 24608)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     The sequence is a part of the data (ACCESSION No. AP000165 -
            AP000173).
            The sequencing project is supported by Japan Science Technology
            Corporation (JST) and The Institute of Physical and Chemical
            Research (RIKEN).
FEATURES             Location/Qualifiers
     source          1. .24608
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
                     /clone="Q12C8"
BASE COUNT      6797 a   5420 c   5437 g   6954 t
ORIGIN

  Query Match            100.0%;  Score 369;  DB 9;  Length 24608;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-100;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15696 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 15755

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15756 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 15815

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15816 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 15875

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15876 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 15935

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15936 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 15995

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15996 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 16055

Qy     361 ATGTCCCCC 369
          |||||||||
Db   16056 ATGTCCCCC 16064


RESULT 5
AP000052
LOCUS       AP000052              100000 bp    DNA     linear   PRI 20-NOV-1999
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28,
            complete sequence.
ACCESSION   AP000052
VERSION     AP000052.1  GI:3132362
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:245P17-f4A4f_2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA, chromosome 21q
```

```
  JOURNAL   Published Only in DataBase (1998)
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-1998) Masahira Hattori, Kitasato University,
            Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
            Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
            Tel:0427-78-9732, Fax:0427-78-9561)
COMMENT     This sequence is conducted by Kitasato University JST sequencing
            Laboratory as a JST sequencing team.
            Principal Investigator:Yoshiyuki Sakaki Ph.D.
            Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
            sakaki@hgc.ims.u-tokyo.ac.jp
            Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
            sequence is submitted by:Human Genome Sequencing in ALIS project of
            JST
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0028 Japan
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top. html)
            or send email to webmaster@www-alis.tokyo.jst.go.jp'.
FEATURES             Location/Qualifiers
     source          1. .100000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
                     /clone="245P17-f4A4f_2"
BASE COUNT    27603 a  21934 c  22513 g  27950 t
ORIGIN

  Query Match             100.0%;  Score 369;  DB 9;  Length 100000;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-100;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80218 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 80277

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80278 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 80337

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80338 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 80397

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80398 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 80457

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80458 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 80517

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80518 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 80577

Qy    361 ATGTCCCCC 369
          |||||||||
Db  80578 ATGTCCCCC 80586


RESULT 6
AP000167
LOCUS       AP000167              100000 bp    DNA     linear   PRI 08-JAN-2000
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
            clone B2344F14-f50E8, segment 3/9, complete sequence.
ACCESSION   AP000167
VERSION     AP000167.1  GI:4827132
KEYWORDS    HTG.
```

```
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Homo sapiens 890,291bp genomic DNA of 21q22.1 (REGION: D21S226-AML
            CLONE RANGE: B2344F14-f50E8)
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     E. coli transposon insertion:The present data does not contain E.
            coli transposon sequences which integrated in the
            original/previous sequences.  We determined the boundary between
            the insertion and genomic sequences experimentally, removed the
            insertion sequences, reconstituted the present data. The sequencing
            project is supported by Japan Science Technology Corporation (JST)
            and The Institute of Physical and Chemical Research (RIKEN).
FEATURES             Location/Qualifiers
     source          1. .100000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
BASE COUNT    27338 a  22306 c  22571 g  27785 t
ORIGIN

  Query Match             100.0%;  Score 369;  DB 9;  Length 100000;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-100;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72186 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 72245

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72246 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 72305

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72306 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 72365

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72366 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 72425

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72426 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 72485

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72486 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 72545

Qy    361 ATGTCCCCC 369
          |||||||||
Db  72546 ATGTCCCCC 72554


RESULT 7
AP000120
ID   AP000120   standard; DNA; HUM; 100000 BP.
XX
```

```
AC   AP000120;
XX
SV   AP000120.1
XX
DT   04-MAY-1999 (Rel. 59, Created)
DT   26-SEP-1999 (Rel. 61, Last updated, Version 3)
XX
DE   Homo sapiens genomic DNA of 21q22.1, GART and AML related, SLC5A3-f4A4
DE   region, segment 3/8.
XX
KW   HTG.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-100000
RA   Hirakawa M., Yamaguchi H., Imai K., Shimada J.;
RT   ;
RL   Submitted (15-APR-1999) to the EMBL/GenBank/DDBJ databases.
RL   Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced
RL   Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan
RL   (E-mail:mika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/,
RL   Tel:81-3-5214-8491, Fax:81-3-5214-8470)
XX
RN   [2]
RA   Hattori M., Ishii K., Toyoda A., Shiba T., Sakaki Y.;
RT   "Homo sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region";
RL   Unpublished.
XX
CC   This sequence is conducted by Kitasato University JST sequencing
CC   Laboratory as a JST sequencing team.
CC   Principal Investigator:Yoshiyuki Sakaki Ph.D.
CC   Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
CC   sakaki@hgc.ims.u-tokyo.ac.jp
CC   Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
CC   The sequence is submitted by Human Genome Sequencing in ALIS
CC   project of JST.
CC   Japan Science and Technology Corporation (JST)
CC   5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
CC   For further information about this sequence, including its
CC   location and relationship to other sequences, please visit our
CC   sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/)
CC   or send email to webmaster@www-alis.tokyo.jst.go.jp
XX
FH   Key             Location/Qualifiers
FH
FT   source          1. .100000
FT                   /chromosome="21"
FT                   /db_xref="taxon:9606"
FT                   /sequenced_mol="DNA"
FT                   /organism="Homo sapiens"
FT                   /map="21q22.1"
FT   STS             32213. .32320
FT                   /note="83F9aL-F/83F9aL-R;The location is between each
FT                   flanking site of PCR primers."
FT                   /standard_name="D21S1689"
FT   STS             43934. .44157
FT                   /note="AFMa086yf9;Genethon Marker;The location is between
FT                   each flanking site of PCR primers."
FT                   /standard_name="D21S1920"
XX
SQ   Sequence 100000 BP; 27731 A; 21990 C; 22220 G; 28059 T; 0 other;

  Query Match             100.0%;  Score 369;  DB 17;  Length 100000;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-100;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89520 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 89579

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89580 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 89639

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89640 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 89699

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89700 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 89759

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89760 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 89819

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89820 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 89879

Qy     361 ATGTCCCCC 369
          |||||||||
Db   89880 ATGTCCCCC 89888


RESULT 8
AP001719
LOCUS       AP001719               340000 bp    DNA     linear   PRI 10-MAY-2000
DEFINITION  Homo sapiens genomic DNA, chromosome 21q, section 63/105.
ACCESSION   AP001719 AL163264 BA000005
VERSION     AP001719.1  GI:7768719
KEYWORDS    .
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
            Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
            Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
            Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
            Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
            Asakawa,S., Shintani,A., Sasaki,K., Nagamine,K., Mitsuyama,S.,
            Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
            Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
            Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
            Hennig,S., Riesselmann,L., Dagand,E., Wehrmeyer,S., Borzym,K.,
            Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
            Yaspo,M.L.
  TITLE     The DNA sequence of human chromosome 21
  JOURNAL   Nature 405 (6784), 311-319 (2000)
  MEDLINE   20289799
REFERENCE   2  (bases 1 to 340000)
  AUTHORS   Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
            Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
            Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
            Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
            Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
            Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
            Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
            Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
            Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
            Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
            Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
            Yaspo,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
            Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
            Group * Institute of Molecular Biotechnology, Genome Analysis *
            Keio University School of Medicine, Dept. of Molecular Biology *
            GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular
```

```
            Genetics (addresses see below)
COMMENT     On May 30, 2000 this sequence version replaced gi:7717333.
            The chromosome 21 mapping and sequencing consortium consisting of
            * RIKEN Genomic Sciences Center, Human Genome Research Group, *
            Sagamihara 228-8555, Japan,
            * e.mail: hattori@gsc.riken.go.jp
            * URL: http://hgp.gsc.riken.go.jp/
            and
            * Institute of Molecular Biotechnology, Genome Analysis, *
            Beutenbergstrasse 11, D-07745 Jena, Germany,
            * e.mail: gscj-submit@genome.imb-jena.de
            * URL: http://genome.imb-jena.de/
            and
            * Keio University School of Medicine, Molecular Biology, * Tokyo
            160-8582, Japan,
            * e.mail: nshimizu@dmb-med.keio.ac.jp
            * URL: http://www.dmb.med.keio.ac.jp/
            and
            * GBF, Dept. of Genome Analysis,
            * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
            info.genome@gbf.de
            * URL: http://genome.gbf.de/
            and
            * Max-Planck Institute for Molecular Genetics,
            * Ihnestrasse 73, D-14195 Berlin, Germany,
            * e.mail: info-chr21@molgen.mpg.de
            * URL: http://chr21.rz-berlin.mpg.de/
            AL163264: Submitted (10-Apr-2000).
FEATURES                Location/Qualifiers
     source             1. .340000
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
     source             <1. .29420
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="R338L7, 5' partial"
                        /clone_lib="RPCI-11 BAC library"
                        /note="Accession No. AP000467"
     source             29242. .97350
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="CTD2344F14"
                        /clone_lib="CTD BAC library"
                        /note="Accession No. AP000315"
     source             96883. .121400
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="pS185"
                        /clone_lib="CMP21 P1 library"
                        /note="Accession No. AP000316"
     source             121210. .218631
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="P245P17"
                        /clone_lib="RP1 PAC library"
                        /note="Accession No. AP000317"
     source             218558. .260079
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="pQ6F8"
                        /clone_lib="CMP21 P1 library"
                        /note="Accession No. AP000318"
     source             258735. .285904
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="pQ94A10"
                        /clone_lib="CMP21 P1 library"
                        /note="Accession No. AP000319"
     source             285732. .310339
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="pQ12C8"
                        /clone_lib="CMP21 P1 library"
                        /note="Accession No. AP000320"
     source             310050. .326194
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="pQ82F5"
                        /clone_lib="CMP21 P1 library"
                        /note="Accession No. AP000321"
     source             325966. .>340000
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="21"
                        /map="21q22.1"
                        /clone="pQ97G8, 3' partial"
                        /clone_lib="CMP21 P1 library"
                        /note="Accession No. AP000322"
     repeat_region      complement(1382. .1688)
                        /note="AluSp"
                        /rpt_family="SINE/Alu"
                        /rpt_type=DISPERSED
     repeat_region      complement(2099. .2390)
                        /note="AluSx"
                        /rpt_family="SINE/Alu"
                        /rpt_type=DISPERSED
     repeat_region      2799. .2884
                        /note="MIR"
                        /rpt_family="SINE/MIR"
                        /rpt_type=DISPERSED
     repeat_region      complement(2891. .3287)
                        /note="MER31A"
                        /rpt_family="LTR/MER4-group"
                        /rpt_type=DISPERSED
     repeat_region      3288. .3381
                        /note="MIR"
                        /rpt_family="SINE/MIR"
                        /rpt_type=DISPERSED
     misc_feature       4211. .5231
                        /note="CpG island"
     misc_feature       4272. .4279
                        /note="NotI site"
     repeat_region      4328. .4476
                        /note="(CGGGG)n"
                        /rpt_family="Simple_repeat"
                        /rpt_type=TANDEM
     gene               4392. .35127
                        /gene="SLC5A3"
     mRNA               join(4392. .4740,12254. .35127)
                        /gene="SLC5A3"
                        /product="Sodium/myo-inositol cotransporter"
                        /note="human solute carrier family 5, member 3, Accession
                        No. AF027153"
     exon               4392. .4740
                        /gene="SLC5A3"
                        /number=1
     misc_feature       4392. .4399
                        /gene="SLC5A3"
                        /note="NotI site"
```

```
     repeat_region   4810. .4985
                     /note="(CGGG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM
     repeat_region   5099. .5191
                     /note="(CCG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM

  Query Match             100.0%;  Score 369;  DB 9;  Length 340000;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-100;
  Matches  369;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301427 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 301486

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301487 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 301546

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301547 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 301606

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301607 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 301666

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301667 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 301726

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301727 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 301786

Qy    361 ATGTCCCCC 369
          |||||||||
Db 301787 ATGTCCCCC 301795


RESULT 9
AX406939
LOCUS       AX406939                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 1 from Patent WO0222875.
ACCESSION   AX406939
VERSION     AX406939.1  GI:21439814
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 1 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Val substitued for Ala at
                     amino acid 116"
                     /codon_start=1
                     /protein_id="CAD35310.1"
                     /db_xref="GI:21439815"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGVAGFKMSP"
     variation       420
                     /note="The drug associated here was quinidine."
                     /replace="c"
BASE COUNT      221 a    151 c    157 g    203 t
ORIGIN

  Query Match             99.6%;  Score 367.4;  DB 6;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-100;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGTGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCC 369
          |||||||||
Db    434 ATGTCCCCC 442


RESULT 10
AX406943
LOCUS       AX406943                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 5 from Patent WO0222875.
ACCESSION   AX406943
VERSION     AX406943.1  GI:21439818
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 5 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Thr substitued for Met at
                     amino acid 54"
                     /codon_start=1
                     /protein_id="CAD35181.1"
                     /db_xref="GI:21439819"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLTVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
     variation       234
                     /note="The drug associated here was procainamide."
                     /replace="t"
BASE COUNT      221 a    153 c    157 g    201 t
ORIGIN

  Query Match             99.6%;  Score 367.4;  DB 6;  Length 732;
```

```
  Best Local Similarity   99.7%;  Pred. No. 2.6e-100;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCACGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
           |||||||||
Db     434 ATGTCCCCC 442


RESULT 11
AX406945
LOCUS       AX406945                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 7 from Patent WO0222875.
ACCESSION   AX406945
VERSION     AX406945.1  GI:21439820
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 7 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Thr substituted for Ile at
                     amino acid 57"
                     /codon_start=1
                     /protein_id="CAD35311.1"
                     /db_xref="GI:21439821"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMTGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
     variation       243
                     /note="The drug associated here was oxatomide."
                     /replace="t"
BASE COUNT      221 a    153 c    157 g    201 t
ORIGIN

  Query Match             99.6%;  Score 367.4;  DB 6;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-100;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGACTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCC 369
           |||||||||
Db     434 ATGTCCCCC 442


RESULT 12
AX406947
LOCUS       AX406947                732 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 9 from Patent WO0222875.
ACCESSION   AX406947
VERSION     AX406947.1  GI:21439822
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldstein,S.A.
  TITLE     Polymorphisms associated with cardiac arrythmia
  JOURNAL   Patent: WO 0222875-A 9 21-MAR-2002;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             74. .445
                     /note="minK-related peptide 1, Ala substitued for Thr at
                     amino acid 8"
                     /codon_start=1
                     /protein_id="CAD35312.1"
                     /db_xref="GI:21439823"
                     /translation="MSTLSNFAQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
     variation       95
                     /note="The drug associated here is was Bactrim."
                     /replace="a"
BASE COUNT      220 a    152 c    158 g    202 t
ORIGIN

  Query Match             99.6%;  Score 367.4;  DB 6;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-100;
  Matches  368;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCGCACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193
```

```
Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCC 369
          |||||||||
Db    434 ATGTCCCCC 442
```

```
RESULT 13
BC022699
LOCUS       BC022699               1664 bp    mRNA    linear   ROD 07-AUG-2002
DEFINITION  Mus musculus, RIKEN cDNA 2200002I16 gene, clone MGC:31447
            IMAGE:4481325, mRNA, complete cds.
ACCESSION   BC022699
VERSION     BC022699.1  GI:18490550
KEYWORDS    MGC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1664)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 44 Row: a Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES             Location/Qualifiers
     source          1. .1664
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="MGC:31447 IMAGE:4481325"
                     /tissue_type="Eye, retina, mouse strain C57Bl\6"
                     /clone_lib="NIH_MGC_94"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             90. .461
                     /codon_start=1
                     /product="RIKEN cDNA 2200002I16 gene"
                     /protein_id="AAH22699.1"
                     /db_xref="GI:18490551"
                     /db_xref="LocusID:69143"
                     /translation="MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAE
                     NFYYVILYLMVMIGMFSFIVVAILVSTVKSKRREHSQHPYHQYIVEDWQEKYKSQILH
                     LEDSKATIHENMGATGFTVSP"
BASE COUNT      502 a    337 c    404 g    421 t
ORIGIN
```

```
  Query Match             71.8%;  Score 265;  DB 10;  Length 1664;
  Best Local Similarity   82.4%;  Pred. No. 3.6e-69;
  Matches  304;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | || ||| ||||||| || ||||| ||||| || | |||| || ||||||||||
Db     90 ATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAAAAAGATTTTTATT 149

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||  ||| |   |||||| |||| ||| |  |||| |||| |||| |
Db    150 ACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGCACTCCAGGCCAGA 209

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| |||||||||||||| ||||||||||||||||||||||||||| || ||||||
Db    210 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 269

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          || |||||| | |||||||||||||||||||| ||||| || ||| | || || ||||||
Db    270 TCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGAGAGCACTCC 329

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
            |  |||| |||||||||||||| || || || |||||||||||||||||| || || |||
Db    330 CAGCACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTACAAAAGTCAGATC 389

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          || |||| ||||| || |||||||||||||||||||||||| || ||| | ||||||| |
Db    390 CTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACATGGGGGCGACGGGGTTCACA 449

Qy    361 ATGTCCCCC 369
          |||| |||
Db    450 GTGTCACCC 458
```

```
RESULT 14
AY050513
LOCUS       AY050513               372 bp    mRNA    linear   ROD 15-OCT-2001
DEFINITION  Cavia porcellus minK-related peptide 1 mRNA, complete cds.
ACCESSION   AY050513
VERSION     AY050513.1  GI:16151156
KEYWORDS    .
SOURCE      Cavia porcellus.
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Jiang,M., Zhang,M., Liu,J. and Tseng,G.-N.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-2001) Physiology, Virginia Commonwealth
            University, 1101 East Marshall Street, Richmond, VA 23298, USA
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Cavia porcellus"
                     /db_xref="taxon:10141"
                     /tissue_type="heart"
     CDS             1. .372
                     /note="Mirp1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAL13163.1"
                     /db_xref="GI:16151157"
                     /translation="MTTLANLTQTLEDAFKKVFITYMDSWRRNTTAEQQALQARVDAE
                     NFYYVILYLMVMIGMFAFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILH
                     LEDSKATIHENLGATGFTVSP"
BASE COUNT       95 a     98 c    105 g     74 t
ORIGIN
```

```
  Query Match           71.4%;  Score 263.4;  DB 10;  Length 372;
  Best Local Similarity  82.1%;  Pred. No. 7.9e-69;
  Matches  303;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | |||||| |||| || || ||||| ||||| || | |||| || | |||| |||
Db      1 ATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAAAAGGTTTTCATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          |||||||||||||  ||| |   |||||||||||| || ||| |||| ||||| |||| |
Db     61 ACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCGCTCCAGGCCAGA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| |||||||||||||| |||||||||||||||||||||||| || ||||||
Db    121 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          | |||||| | |||||||||||||||||| ||||| || ||| | ||||| ||||||
Db    181 GCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGGGAGCACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          | ||||| |||||||||||||| || ||||| |||||| | ||||| | ||| || |||
Db    241 CAGGACCCGTACCACCAGTACATCGTGGAGGATTGGCAGCAGAAGTATAGGAGTCAGATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||| |||| ||||| || |||||||||||||||||||| | || ||| | ||||||| |
Db    301 TTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACCTGGGGGCGACGGGGTTCACA 360

Qy    361 ATGTCCCCC 369
          |||| |||
Db    361 GTGTCACCC 369


RESULT 15
AF071003
LOCUS       AF071003                468 bp    mRNA    linear   ROD 29-APR-1999
DEFINITION  Rattus norvegicus minK-related peptide 1 mRNA, complete cds.
ACCESSION   AF071003
VERSION     AF071003.1  GI:4704424
KEYWORDS    .
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Abbott,G.W., Sesti,F., Splawski,I., Buck,M.E., Lehmann,M.H.,
            Timothy,K.W., Keating,M.T. and Goldstein,S.A.
  TITLE     MiRP1 forms IKr potassium channels with HERG and is associated with
            cardiac arrhythmia
  JOURNAL   Cell 97 (2), 175-187 (1999)
  MEDLINE   99235979
   PUBMED   10219239
REFERENCE   2  (bases 1 to 468)
  AUTHORS   Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Section of Developmental Biology and
            Biophysics, Department of Pediatrics and Boyer Center for Molecular
            Medicine, Yale University School of Medicine, 295 Congress Avenue,
            New Haven, CT 06536, USA
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /sex="male"
                     /tissue_type="heart"
                     /dev_stage="10-12 weeks"
     CDS             35. .406
                     /note="potassium channel subunit; MiRP1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAD28087.1"
                     /db_xref="GI:4704425"
                     /translation="MTTLANLTQTLEDAFKKVFITYMDSWRRNTTAEQQALQARVDAE
                     NFYYVILYLMVMIGMFAFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILH
                     LEDSKATIHENLGATGFTVSP"
BASE COUNT      118 a    126 c    131 g     93 t
ORIGIN

  Query Match           71.4%;  Score 263.4;  DB 10;  Length 468;
  Best Local Similarity  82.1%;  Pred. No. 8.3e-69;
  Matches  303;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | |||||| |||| || || ||||| ||||| || | |||| || | |||| |||
Db     35 ATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAAAAGGTTTTCATT 94

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          |||||||||||||  ||| |   |||||||||||| || ||| |||| ||||| |||| |
Db     95 ACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCGCTCCAGGCCAGA 154

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| |||||||||||||| |||||||||||||||||||||||| || ||||||
Db    155 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 214

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          | |||||| | |||||||||||||||||| ||||| || ||| | ||||| ||||||
Db    215 GCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGGGAGCACTCC 274

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          | ||||| |||||||||||||| || ||||| |||||| | ||||| | ||| || |||
Db    275 CAGGACCCGTACCACCAGTACATCGTGGAGGATTGGCAGCAGAAGTATAGGAGTCAGATC 334

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||| |||| ||||| || |||||||||||||||||||| | || ||| | ||||||| |
Db    335 TTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACCTGGGGGCGACGGGGTTCACA 394

Qy    361 ATGTCCCCC 369
          |||| |||
Db    395 GTGTCACCC 403


Search completed: May 21, 2003, 21:21:35
Job time : 1122.35 secs
```

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2003, 14:21:24 ; Search time 44 Seconds
(without alignments)
268.739 Million cell updates/sec

Title: US-09-550-163-2
Perfect score: 632
Sequence: 1 MSTLSNFTQTLEDVFRRIFI.....EESKATIHENIGAAGFKMSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	132.5	21.0	129	1	A32447	potassium channel-
2	128.5	20.3	129	2	S17307	potassium channel
3	128	20.3	130	2	A35633	potassium channel
4	126.5	20.0	125	2	A49392	min K potassium ch
5	126.5	20.0	125	2	I48146	potassium channel-
6	84.5	13.4	439	2	D64510	hypothetical prote
7	76.5	12.1	374	2	T15940	hypothetical prote
8	76.5	12.1	557	2	B47704	probable sensory t
9	75.5	11.9	367	2	E81065	proteinase, probab
10	75.5	11.9	3839	2	T49799	related to TOM1 pr
11	75	11.9	1003	2	AH2335	toxin secretion AB
12	74.5	11.8	1042	2	H70203	isoleucine-tRNA li
13	74	11.7	938	2	T41932	hypothetical prote
14	73.5	11.6	171	2	T41924	hypothetical prote
15	73.5	11.6	497	2	S59103	NADH2 dehydrogenas
16	73.5	11.6	652	2	T41162	hypothetical prote
17	73	11.6	400	2	B64071	tyrosine-specific
18	73	11.6	591	2	AD2148	two-component sens
19	73	11.6	1224	2	E71611	hypothetical prote
20	72.5	11.5	371	2	D89995	accessory gene reg
21	71	11.2	174	2	AG2234	hypothetical prote
22	71	11.2	291	2	A36051	H+/K+-exchanging A
23	70.5	11.2	451	2	F75131	hypothetical prote
24	70.5	11.2	874	2	E82913	valyl-tRNA synthet
25	70	11.1	522	2	C90073	hypothetical prote
26	70	11.1	947	2	G70657	probable adi - Myc
27	70	11.1	1357	2	T16860	hypothetical prote
28	69.5	11.0	554	2	T27878	hypothetical prote
29	69.5	11.0	946	2	S48255	probable membrane
30	69.5	11.0	1154	2	T39663	paired amphipathic
31	69.5	11.0	3973	2	B71612	hypothetical prote
32	69	10.9	282	1	E69906	conserved hypothet
33	69	10.9	548	2	E89910	glycine betaine tr
34	69	10.9	773	2	D90099	hypothetical prote
35	68.5	10.8	350	2	B81803	probable secreted
36	68.5	10.8	655	2	H96692	probable receptor
37	68.5	10.8	696	2	C85047	probable transposo
38	68.5	10.8	701	2	S35313	TIP1 protein - yea
39	68.5	10.8	1007	2	S48535	rho-type GTPase-ac
40	68.5	10.8	1911	2	T43048	calcium channel al
41	68	10.8	303	2	T15694	hypothetical prote
42	68	10.8	378	2	G97301	uncharacterized co
43	68	10.8	435	2	B97516	hypothetical prote
44	68	10.8	435	2	AI2734	ABC transporter, m
45	68	10.8	464	2	T20238	hypothetical prote

ALIGNMENTS

RESULT 1
A32447
potassium channel-activating protein - human
N;Alternate names: delayed rectifier potassium channel
C;Species: Homo sapiens (man)
C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 21-Jul-2000
C;Accession: A32447; I53911
R;Murai, T.; Kakizuka, A.; Takumi, T.; Ohkubo, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 161, 176-181, 1989
A;Title: Molecular cloning and sequence analysis of human genomic DNA encoding a nove
A;Reference number: A32447; MUID:89273632; PMID:2730656
A;Accession: A32447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <MUR>
A;Cross-references: GB:M26685; NID:g186569; PIDN:AAA36129.1; PID:g386838
R;Lai, L.P.; Deng, C.L.; Moss, A.J.; Kass, R.S.; Liang, C.S.
Gene 151, 339-340, 1994
A;Title: Polymorphism of the gene encoding a human minimal potassium ion channel (min
A;Reference number: I53911; MUID:95129890; PMID:7828904
A;Accession: I53911
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37,'G',39-129 <LAI>
A;Cross-references: GB:L33815; NID:g603450; PIDN:AAA63905.1; PID:g603451
C;Genetics:
A;Gene: GDB:KCNE1; ISK
A;Cross-references: GDB:127909; OMIM:176261
A;Map position: 21q22.1-21q22.2
C;Superfamily: human potassium channel-activating protein
C;Keywords: phosphoprotein; transmembrane protein
F;44-66/Domain: transmembrane #status predicted <TMM>

Query Match 21.0%; Score 132.5; DB 1; Length 129;
Best Local Similarity 45.1%; Pred. No. 3.6e-06;
Matches 23; Conservative 15; Mismatches 12; Indels 1; Gaps 1;

Qy 51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKSQI 100
Db 45 LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYV 95

RESULT 2
S17307
potassium channel protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-Dec-1999
C;Accession: S17307; S21135
R;Honore, E.; Attali, B.; Romey, G.; Heurteaux, C.; Ricard, P.; Lesage, F.; Lazdunski
EMBO J. 10, 2805-2811, 1991
A;Title: Cloning, expression, pharmacology and regulation of a delayed rectifier K+
A;Reference number: S17307; MUID:92007723; PMID:1655403

```
A;Accession: S17307
A;Molecule type: mRNA
A;Residues: 1-129 <HON>
A;Cross-references: EMBL:X60457; NID:g52779; PIDN:CAA42990.1; PID:g52780
R;Lesage, F.; Attali, B.; Lazdunski, M.; Barhanin, J.
FEBS Lett. 301, 168-172, 1992
A;Title: I(SK), a slowly activating voltage-sensitive K(+) channel. Characterization of
A;Reference number: S21135; MUID:92233938; PMID:1568475
A;Accession: S21135
A;Molecule type: mRNA
A;Residues: 1-129 <LES>
A;Cross-references: GB:X60457; NID:g52779; PIDN:CAA42990.1; PID:g52780
C;Superfamily: human potassium channel-activating protein
C;Keywords: phosphoprotein; potassium channel; transmembrane protein
F;44-66/Domain: transmembrane #status predicted <TMM>

  Query Match             20.3%;  Score 128.5;  DB 2;  Length 129;
  Best Local Similarity   35.0%;  Pred. No. 9.2e-06;
  Matches   36;  Conservative   22;  Mismatches   28;  Indels   17;  Gaps    6;

Qy      26 WRQNTTAEQ--------EALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRR 77
           |::  ||||          | : |::      ||:::::| | |  : |::| ::||:
Db      17 WQE--TAEQGGNVSGLARKSQLRDDSK---LEALYILMVLGFFGFFTLGIMLSYIRSKKL 71

Qy      78 EHSNDPYHQYIVED-WQEKYKS--QILNLEESKAT-IHENIGA 116
           |||:||:: ||  | |||| |:  |   ||  :|  : ||  |
Db      72 EHSHDPFNVYIESDAWQEKGKAVFQARVLESFRACYVIENQAA 114


RESULT 3
A35633
potassium channel protein - rat
N;Alternate names: I-sK K+ channel protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C;Accession: A35633; A33177; JH0140; I55193
R;Folander, K.; Smith, J.S.; Antanavage, J.; Bennett, C.; Stein, R.B.; Swanson, R.
Proc. Natl. Acad. Sci. U.S.A. 87, 2975-2979, 1990
A;Title: Cloning and expression of the delayed-rectifier I-sK channel from neonatal rat
A;Reference number: A35633; MUID:90222152; PMID:2183220
A;Accession: A35633
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <FOL>
A;Cross-references: GB:M36461; NID:g203976; PIDN:AAA41098.1; PID:g203977
R;Takumi, T.; Ohkubo, H.; Nakanishi, S.
Science 242, 1042-1045, 1988
A;Title: Cloning of a membrane protein that induces a slow voltage-gated potassium curre
A;Reference number: A33177; MUID:89058617; PMID:3194754
A;Accession: A33177
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <TAK>
A;Cross-references: GB:M22412; NID:g206051; PIDN:AAA41822.1; PID:g206052
R;Pragnell, M.; Snay, K.J.; Trimmer, J.S.; MacLusky, N.J.; Naftolin, F.; Kaczmarek, L.K.
Neuron 4, 807-812, 1990
A;Title: Estrogen induction of a small, putative K+ channel mRNA in rat uterus.
A;Reference number: JH0140; MUID:90262731; PMID:2344412
A;Accession: JH0140
A;Molecule type: mRNA
A;Residues: 1-130 <PRA>
A;Experimental source: uterus
R;Iwai, M.; Masu, M.; Tsuchida, K.; Mori, T.; Ohkubo, H.; Nakanishi, S.
J. Biochem. 108, 200-206, 1990
A;Title: Characterization of gene organization and generation of heterogeneous mRNA spec
A;Reference number: I55193; MUID:91035347; PMID:2229022
A;Accession: I55193
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:D10708; NID:g220908; PIDN:BAA01552.1; PID:g2160466
C;Superfamily: human potassium channel-activating protein
C;Keywords: phosphoprotein; transmembrane protein
F;45-67/Region: hydrophobic

  Query Match             20.3%;  Score 128;  DB 2;  Length 130;
  Best Local Similarity   41.4%;  Pred. No. 1e-05;
  Matches   29;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    3;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS--QILNLEESK 107
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:  |   ||  :
Db      46 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDAWQEKGKALFQARVLESFR 105

Qy     108 AT-IHENIGA 116
           |  : ||  |
Db     106 ACYVIENQAA 115


RESULT 4
A49392
min K potassium channel, gpIsK - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C;Accession: A49392
R;Varnum, M.D.; Busch, A.E.; Bond, C.T.; Maylie, J.; Adelman, J.P.
Proc. Natl. Acad. Sci. U.S.A. 90, 11528-11532, 1993
A;Title: The min K channel underlies the cardiac potassium current IKs and mediates s
A;Reference number: A49392; MUID:94089666; PMID:8265583
A;Accession: A49392
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-125 <VAR>
A;Experimental source: heart
A;Note: sequence extracted from NCBI backbone (NCBIP:140983)
C;Superfamily: human potassium channel-activating protein

  Query Match             20.0%;  Score 126.5;  DB 2;  Length 125;
  Best Local Similarity   44.9%;  Pred. No. 1.4e-05;
  Matches   22;  Conservative   15;  Mismatches   11;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS 98
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:
Db      45 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDTWQEKDKA 93


RESULT 5
I48146
potassium channel-activating protein - Cavia cobaya
C;Species: Cavia cobaya
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 31-Jan-2000
C;Accession: I48146
R;Zhang, J.; Jurkiewicz, N.K.; Folander, K.; Lazarides, E.; Salata, J.J.; Swanson, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 1766-1770, 1994
A;Title: K+ currents expressed from the guinea pig cardiac IsK protein are enhanced b
A;Reference number: A53135; MUID:94173910; PMID:7510407
A;Accession: I48146
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-125 <RES>
A;Cross-references: GB:L20462; NID:g484140; PIDN:AAA72394.1; PID:g484141
C;Superfamily: human potassium channel-activating protein

  Query Match             20.0%;  Score 126.5;  DB 2;  Length 125;
  Best Local Similarity   44.9%;  Pred. No. 1.4e-05;
  Matches   22;  Conservative   15;  Mismatches   11;  Indels    1;  Gaps    1;

Qy      51 LYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVED-WQEKYKS 98
           ||:::::| | |  : |::| ::||: |||:||:: ||  | |||| |:
Db      45 LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDTWQEKDKA 93


RESULT 6
D64510
hypothetical protein MJECL04 - Methanococcus jannaschii plasmid pURB800
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 08-Oct-1999
```

```
C;Accession: D64510
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64510
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-439 <BUL>
A;Cross-references: GB:L77118; NID:g1500644; TIGR:MJECL04; PIDN:AAC37078.1; PID:g1500652
C;Genetics:
A;Map position: ECLFOR1934-3253
A;Genome: plasmid
A;Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromosc
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH19

  Query Match             13.4%;  Score 84.5;  DB 2;  Length 439;
  Best Local Similarity   23.3%;  Pred. No. 0.92;
  Matches   24;  Conservative   19;  Mismatches   31;  Indels   29;  Gaps    3;

Qy      33 EQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREH---------- 79
           | :||  |:|: || ::::|    ||     : ::       : |||
Db       8 ELKALNEKLDSNNFEFIVIYGRRRIGKTKLALKSV-------ENREHIYYLAVEGDNLKH 60

Qy      80 ------SNDPYHQYIVEDWQEKY---KSQILNLEESKATIHEN 113
                :|  :|  |||:  :   | :|: ::|    | ||
Db      61 FKRYASKVEPTIEYAKEDWEAYFNFLKDKIIIIDEFPNLIKEN 103


RESULT 7
T15940
hypothetical protein F01E11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15940
R;Geisel, C.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F01E11.
A;Reference number: Z18434
A;Accession: T15940
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-374 <GEI>
A;Cross-references: EMBL:U42832; NID:g1125742; PID:g1125746; PIDN:AAA83573.1; CESP:F01E1
C;Genetics:
A;Gene: CESP:F01E11.4
A;Introns: 76/1; 104/3; 193/3; 229/3; 244/1; 256/2; 282/1; 328/2

  Query Match             12.1%;  Score 76.5;  DB 2;  Length 374;
  Best Local Similarity   19.7%;  Pred. No. 4.9;
  Matches   29;  Conservative   20;  Mismatches   41;  Indels   57;  Gaps    4;

Qy      31 TAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIVAI---------------------- 67
           |  : :  | |   |      ||:::::|: ||::  :
Db     117 TLREVSFTASVIGTNLIVYCPYLLILVGILSFVMTPVRFFSIILNDNKIMITHMFATIFF 176

Qy      68 -------------LVSTVKSKRREH---------SNDPYHQYIVEDWQEKYKS----QIL 101
                       | | | |   ||           :|   :|:|:| : ::      :
Db     177 ATICAMTAILGYDLNSHVSSSDMEHWMKHSIKEDYGNPTAPHIMEEWNKAHRQFKCCGVR 236

Qy     102 NLEE--------SKATIHENIGAAGFK 120
           || :        | ||:||    | ||
Db     237 NLTDFVENSCCASCATMHERFCVAFFK 263


RESULT 8
B47704 .
probable sensory transducer protein - Clostridium thermocellum
C;Species: Clostridium thermocellum
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C;Accession: B47704
R;Hazlewood, G.P.; Davidson, K.; Laurie, J.I.; Huskisson, N.S.; Gilbert, H.J.
J. Gen. Microbiol. 139, 307-316, 1993
A;Title: Gene sequence and properties of CelI, a family E endoglucanase from Clostri
A;Reference number: A47704; MUID:93171873; PMID:8436949
A;Accession: B47704
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-557 <HAZ>
A;Cross-references: GB:L04736; NID:g144912; PIDN:AAA20891.1; PID:g144913
A;Note: sequence extracted from NCBI backbone (NCBIP:125641)
C;Superfamily: methyl-accepting chemotaxis protein
C;Keywords: transmembrane protein

  Query Match             12.1%;  Score 76.5;  DB 2;  Length 557;
  Best Local Similarity   23.2%;  Pred. No. 7.6;
  Matches   29;  Conservative   24;  Mismatches   47;  Indels   25;  Gaps    5;

Qy       1 MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMF 60
           :| : :   || | |   |: |      |||| :| :       :    :: ::: :|:
Db      84 LSDIDDIGDTLRDYF-EAFVEY------NTTAAKEKVDENKQVASTASTVMIVVIFVGIL 136

Qy      61 SFIIVAILVSTVKSKRREHSNDPYHQYI----------VE-DWQEKYKSQILNLEESKAT 109
              | : : :| : ||       |  | :          || | : : : :|  | ||
Db     137 IAIALGVFISRIISK-------PIGQMVEAADRLALGDVEVDVKAETRDEIGKLAESFKR 189

Qy     110 IHENI 114
           : |||
Db     190 MIENI 194


RESULT 9
E81065
proteinase, probable NMB1587 [imported] - Neisseria meningitidis (strain MC58 serogrc
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: E81065
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.,
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81065
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <TET>
A;Cross-references: GB:AE002509; GB:AE002098; NID:g7226832; PIDN:AAF41940.1; PID:g722
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1587

  Query Match             11.9%;  Score 75.5;  DB 2;  Length 367;
  Best Local Similarity   29.8%;  Pred. No. 6.1;
  Matches   25;  Conservative   17;  Mismatches   25;  Indels   17;  Gaps    4;

Qy      33 EQEALQA--KVDAENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVE 90
           ||| :|:  |    |:   :| |: : |  : |::||    |:||::  |       ::
Db      11 EQEEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAI----VQSKKQSESG----SVVLT 62

Qy      91 DWQEKYKSQ-------ILNLEESK 107
           |: | || |         |: ||:|
Db      63 DFSENYKKQRQSFEAFFLSGEEAK 86


RESULT 10
T49799
related to TOM1 protein [imported] - Neurospora crassa
N;Alternate names: protein B11B22.10
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49799
```

```
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49799
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3839 <SCH>
A;Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.10
A;Experimental source: BAC clone B11B22; strain OR74A
C;Genetics:
A;Gene: NCSP:B11B22.10
A;Map position: 6
A;Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1

  Query Match             11.9%;  Score 75.5;  DB 2;  Length 3839;
  Best Local Similarity   24.6%;  Pred. No. 81;
  Matches   29;  Conservative   21;  Mismatches   49;  Indels   19;  Gaps    3;

Qy       6 NFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSFIIV 65
Db    2869 NAEQQAEDERPRVYYTLRNQ-------QIDITELGIDAE-------YLEALPEEFRDEVI 2914

Qy      66 AILVSTVKSKRREH-----SNDPYHQYIVEDWQEKYKSQILNLEESKATIHENIGAAG 118
Db    2915 AQAISTRRSQAREQVSQEGENTEVFQEFLEALPEELRNEILHQEQHEQRRRERQNAAG 2972


RESULT 11
AH2335
toxin secretion ABC transporter ATP-binding protein alr4239 [imported] - Nostoc sp. (str
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AH2335
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2335
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1003 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75938.1; PID:g17133374; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4239
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

  Query Match             11.9%;  Score 75;  DB 2;  Length 1003;
  Best Local Similarity   23.0%;  Pred. No. 21;
  Matches   31;  Conservative   20;  Mismatches   30;  Indels   54;  Gaps    7;

Qy      20 ITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVM---------IGMFS---FIIVAI 67
Db     548 INELENIRQFLTG--TALTVGLDA---VFSVVYIIVMLFYSWQLTLVGLGTIPIFIIITL 602

Qy      68 LVSTVKSKR---REHSNDPYHQYIVE------------------DWQEKYKSQILNLEE 105
Db     603 IASPTVSRQLRSKAERNSETQSYLVEVMSGIQTVKAQNIELRSRFSWQERYARYV----- 657

Qy     106 SKATIHENIGAAGFK 120
Db     658 ----------AAGFK 662


RESULT 12
H70203
isoleucine-tRNA ligase (EC 6.1.1.5) ileS - Lyme disease spirochete
N;Alternate names: isoleucyl-tRNA synthetase
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
C;Accession: H70203
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70203
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1042 <KLE>
A;Cross-references: GB:AE001181; GB:AE000783; NID:g2688772; PIDN:AAC67179.1; PID:g268
A;Experimental source: strain B31
C;Superfamily: isoleucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

  Query Match             11.8%;  Score 74.5;  DB 2;  Length 1042;
  Best Local Similarity   27.3%;  Pred. No. 24;
  Matches   33;  Conservative   24;  Mismatches   45;  Indels   19;  Gaps    8;

Qy       6 NFTQTLEDVFRRIFITYMDNW------RQNTTAEQEALQAKVDA-ENFYYVILYLMVMIG 58
Db     703 NLTKSIESLLE--FIDKLNNWYIRRSRRRFWKSEND--KDKNDAYETLYYAIKTLMILLA 758

Qy      59 MF-SFIIVAIL--VSTVKSKRREHSND---PYHQYIVEDWQEKYK--SQILNLEESKATI 110
Db     759 PFIPFITEEIYQNLKTDEDKQSIHLNDYPKANENFINKTIEEKINLARKITSMARSLRSL 818

Qy     111 H 111
Db     819 H 819


RESULT 13
T41932
hypothetical protein U30 - human herpesvirus 7 (strain JI)
C;Species: human herpesvirus 7
A;Variety: strain JI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41932
R;Nicholas, J.
submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the complete nucleotide sequence of huma
A;Reference number: Z22022
A;Accession: T41932
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-938 <NIC>
A;Cross-references: EMBL:U43400; PIDN:AAC54692.1
A;Experimental source: strain JI
C;Genetics:
A;Note: U30

  Query Match             11.7%;  Score 74;  DB 2;  Length 938;
  Best Local Similarity   27.0%;  Pred. No. 24;
  Matches   30;  Conservative   19;  Mismatches   56;  Indels    6;  Gaps    4;

Qy       3 TLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAENFYYVILYLMVMIGMFSF 62
Db     773 TLQNFIIIVERISSHANTTYQDVLNSIDECHFSNMQLIQSFKNIVYVIDVLNTK-NIFNF 831

Qy      63 IIVAILVSTVKSKRREHSNDPYHQY-IVEDWQEKYKSQILNL-EESKATIH 111
Db     832 SLASQLIEAKKLVKKQ---DTYNQLNVQDDFVTVLKSHLNNLFEKQKPTIN 879


RESULT 14
T41924
hypothetical protein U23 - human herpesvirus 7 (strain JI)
C;Species: human herpesvirus 7
A;Variety: strain JI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41924
```

```
R;Nicholas, J.
submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the complete nucleotide sequence of human h
A;Reference number: Z22022
A;Accession: T41924
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-171 <NIC>
A;Cross-references: EMBL:U43400; PIDN:AAC54684.1
A;Experimental source: strain JI
C;Genetics:
A;Note: U23

  Query Match             11.6%;  Score 73.5;  DB 2;  Length 171;
  Best Local Similarity   36.6%;  Pred. No. 4.2;
  Matches   15;  Conservative   11;  Mismatches   12;  Indels    3;  Gaps    1;

Qy      50 ILYLMVMIGMFSFI---IVAILVSTVKSKRREHSNDPYHQY 87
           :|:|:::|   |||    :|:||  :|: :| ||  | : |
Db     121 VLFLVILIAAVSFIGIVALALLVLLIKNPKRNHSKKPKNAY 161


RESULT 15
S59103
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - red alga (Chondrus crispus) mito
C;Species: mitochondrion Chondrus crispus (carragheen)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 03-Jun-2002
C;Accession: S59103
R;Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienenberger, J.M.; Kloareg, B.
J. Mol. Biol. 250, 484-495, 1995
A;Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus (
A;Reference number: S59078; MUID:95341681; PMID:7616569
A;Accession: S59103
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-497 <LEB>
A;Cross-references: EMBL:Z47547; NID:g1019057; PIDN:CAA87619.1; PID:g1334497
A;Experimental source: female gametophytes
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C;Genetics:
A;Gene: nad2
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Function:
A;Description: oxidation of NADH and reduction of ubiquinone coupled to proton transport
A;Pathway: respiratory chain
A;Note: FAD cofactor
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: FAD; iron-sulfur protein; membrane-associated complex; mitochondrion; NAD; c

  Query Match             11.6%;  Score 73.5;  DB 2;  Length 497;
  Best Local Similarity   26.2%;  Pred. No. 13;
  Matches   16;  Conservative   14;  Mismatches   14;  Indels   17;  Gaps    2;

Qy      43 AENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN 102
           : : :|||:|:: |:|:|||:                |  ||      :| :|   :::
Db     335 SSSIFYVIIYVITMLGIFSFILTL----------RFYNYSYH------YQTRYLQDLIS 377

Qy     103 L 103
           |
Db     378 L 378


Search completed: May 15, 2003, 14:25:36
Job time : 47 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2002, 13:15:00 ; Search time 1800 Seconds
(without alignments)
4324.818 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_445
Perfect score: 372
Sequence: 1 atgtctactttatccaatttt.....ggttcaaaatgtccccctga 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	372	100.0	732	9	AF071002	AF071002 Homo sapi
2	372	100.0	809	9	AF302095	AF302095 Homo sapi
3	372	100.0	24608	9	AP000320	AP000320 Homo sapi
4	372	100.0	100000	9	AP000052	AP000052 Homo sapi
5	372	100.0	100000	9	AP000120	AP000120 Homo sapi
6	372	100.0	100000	9	AP000167	AP000167 Homo sapi
7	372	100.0	340000	9	AP001719	AP001719 Homo sapi
8	268	72.0	1664	10	BC022699	BC022699 Mus muscu
9	266.4	71.6	372	10	AY050513	AY050513 Cavia por
10	266.4	71.6	468	10	AF071003	AF071003 Rattus no
11	186.2	50.1	215	4	AF329636	AF329636 Oryctolag
12	178.2	47.9	228	4	AF387764	AF387764 Equus cab
13	56	15.1	534	4	RABIPCS	L41659 Oryctolagus
14	55	14.8	750	10	GPIISK	L20462 Cavia cobay
15	53.2	14.3	390	9	AF135188	AF135188 Homo sapi
16	53.2	14.3	390	10	AY050512	AY050512 Cavia por
17	53.2	14.3	398	6	I40373	I40373 Sequence 5
18	53.2	14.3	402	9	HUMISKA	L33815 Homo sapien
19	53.2	14.3	408	9	HUMCDRPCA	L28168 Homo sapien
20	53.2	14.3	436	9	HUMISK	M26685 Human IsK p
21	53.2	14.3	1703	6	AR119312	AR119312 Sequence
22	53.2	14.3	1703	6	AR164693	AR164693 Sequence
c 23	53.2	14.3	43126	9	AP000324	AP000324 Homo sapi
c 24	53.2	14.3	100000	9	AP000053	AP000053 Homo sapi
c 25	53.2	14.3	100000	9	AP000121	AP000121 Homo sapi
c 26	53.2	14.3	100000	9	AP000168	AP000168 Homo sapi
c 27	53.2	14.3	340000	9	AP001720	AP001720 Homo sapi
28	52.8	14.2	611	10	MMKCHA	X60457 M.musculus
29	52.6	14.1	393	4	AB032575	AB032575 Sus scrof
30	51	13.7	471	10	RATDRTKCA	M36461 Rat delayed
31	51	13.7	585	10	RATPCPA	M22412 Rat potassi
32	50.4	13.5	390	4	MSU62404	U62404 Felis catus
33	44.6	12.0	422	12	SYNMINK	M64922 Synthetic v
c 34	41	11.0	6408	6	AX346023	AX346023 Sequence
c 35	39	10.5	161482	2	AP004643	AP004643 Oryza sat
36	38.6	10.4	4881	3	DSPTEH2	X60437 Drosophila
37	38.2	10.3	166856	2	AC011944	AC011944 Homo sapi
38	38.2	10.3	177045	2	AC015970	AC015970 Homo sapi
c 39	38.2	10.3	179522	2	AC104231	AC104231 Homo sapi
40	37.2	10.0	346294	1	AP002999	AP002999 Mesorhizo
41	36.6	9.8	2652	6	A75965	A75965 Sequence 1
42	36.6	9.8	2652	6	I60522	I60522 Sequence 1
43	36.6	9.8	2861	9	S62035	S62035 Ras-specifi
44	36.6	9.8	11488	1	AE005321	AE005321 Escherich
45	36.6	9.8	11749	1	AE000212	AE000212 Escherich

ALIGNMENTS

RESULT 1
AF071002
LOCUS AF071002 732 bp mRNA linear PRI 29-APR-1999
DEFINITION Homo sapiens minK-related peptide 1 mRNA, complete cds.
ACCESSION AF071002
VERSION AF071002.1 GI:4704422
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 732)
AUTHORS Abbott,G.W., Sesti,F., Splawski,I., Buck,M.E., Lehmann,M.H., Timothy,K.W., Keating,M.T. and Goldstein,S.A.
TITLE MiRP1 forms IKr potassium channels with HERG and is associated with cardiac arrhythmia
JOURNAL Cell 97 (2), 175-187 (1999)
MEDLINE 99235979
REFERENCE 2 (bases 1 to 732)
AUTHORS Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-1998) Section of Developmental Biology and Biophysics, Department of Pediatrics and Boyer Center for Molecular

```
           Medicine, Yale University School of Medicine, 295 Congress Avenue,
           New Haven, CT 06536, USA
FEATURES             Location/Qualifiers
     source          1. .732
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q11.1"
                     /tissue_type="heart"
     CDS             74. .445
                     /note="potassium channel subunit; MiRP1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAD28086.1"
                     /db_xref="GI:4704423"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      221 a    152 c    157 g    202 t
ORIGIN

  Query Match           100.0%;  Score 372;  DB 9;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCCTGA 372
          ||||||||||||
Db     434 ATGTCCCCCTGA 445


RESULT 2
AF302095
LOCUS       AF302095                809 bp    mRNA    linear   PRI 14-SEP-2000
DEFINITION  Homo sapiens voltage-gated K+ channel subunit MIRP1 (KCNE2) mRNA,
            complete cds.
ACCESSION   AF302095
VERSION     AF302095.1  GI:10121887
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 809)
  AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
  TITLE     Cloning of human MIRP1 cDNA
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 809)
  AUTHORS   Domenech,A., Estivill,X. and de la Luna,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2000) Medical and Molecular Genetics Center,
            Institut Recerca Oncologica, Avia. de Castelldefels Km 2,7,
            L'Hospitalet de Llobregat, Barcelona 08907, Spain
FEATURES             Location/Qualifiers
     source          1. .809
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22"
     gene            1. .809
                     /gene="KCNE2"
     CDS             141. .512
                     /gene="KCNE2"
                     /codon_start=1
                     /product="voltage-gated K+ channel subunit MIRP1"
                     /protein_id="AAG13416.1"
                     /db_xref="GI:10121888"
                     /translation="MSTLSNFTQTLEDVFRRIFITYMDNWRQNTTAEQEALQAKVDAE
                     NFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQYIVEDWQEKYKSQILN
                     LEESKATIHENIGAAGFKMSP"
BASE COUNT      247 a    172 c    189 g    200 t      1 others
ORIGIN

  Query Match           100.0%;  Score 372;  DB 9;  Length 809;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     141 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 200

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     201 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 260

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     261 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 320

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     321 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 380

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     381 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 440

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     441 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 500

Qy     361 ATGTCCCCCTGA 372
          ||||||||||||
Db     501 ATGTCCCCCTGA 512


RESULT 3
AP000320
LOCUS       AP000320                24608 bp    DNA     linear   PRI 20-NOV-1999
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
            clone:Q12C8, complete sequence.
ACCESSION   AP000320
VERSION     AP000320.1  GI:4835689
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:Q12C8.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24608)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Homo sapiens 24,608bp genomic DNA of 21q22.1
  JOURNAL   Published Only in DataBase (1999) In press
```

```
REFERENCE   2  (bases 1 to 24608)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1999) to the DDBJ/EMBL/GenBank databases.
            Masahira Hattori, The Institute of Physical and Chemical Research
            (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
            Kitasato, Sagamihara, Kanagawa 228-8555, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-42-778-9923, Fax:81-42-778-9924)
COMMENT     The sequence is a part of the data (ACCESSION No. AP000165 -
            AP000173).
            The sequencing project is supported by Japan Science Technology
            Corporation (JST) and The Institute of Physical and Chemical
            Research (RIKEN).
FEATURES             Location/Qualifiers
     source          1. .24608
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /clone="Q12C8"
                     /map="21q22.1"
BASE COUNT     6797 a   5420 c   5437 g   6954 t
ORIGIN

  Query Match             100.0%;  Score 372;  DB 9;  Length 24608;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15696 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 15755

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15756 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 15815

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15816 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 15875

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15876 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 15935

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15936 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 15995

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15996 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 16055

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db  16056 ATGTCCCCCTGA 16067


RESULT 4
AP000052
LOCUS       AP000052              100000 bp    DNA     linear   PRI 20-NOV-1999
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28,
            complete sequence.
ACCESSION   AP000052
VERSION     AP000052.1  GI:3132362
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA, clone:245P17-f4A4f_2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Homo sapiens genomic DNA, chromosome 21q
  JOURNAL   Published Only in DataBase (1998) In press
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAY-1998) to the DDBJ/EMBL/GenBank databases.
            Masahira Hattori, Kitasato University, Department of Science, JST
            Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan
            (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
            Fax:0427-78-9561)
COMMENT     This sequence is conducted by Kitasato University JST sequencing
            Laboratory as a JST sequencing team.
            Principal Investigator:Yoshiyuki Sakaki Ph.D.
            Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
            sakaki@hgc.ims.u-tokyo.ac.jp
            Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
            sequence is submitted by:Human Genome Sequencing in ALIS project of
            JST
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0028 Japan
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top. html)
            or send email to webmaster@www-alis.tokyo.jst.go.jp';.
FEATURES             Location/Qualifiers
     source          1. .100000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /clone="245P17-f4A4f_2"
                     /map="21q22.1"
BASE COUNT     27603 a  21934 c  22513 g  27950 t
ORIGIN

  Query Match             100.0%;  Score 372;  DB 9;  Length 100000;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80218 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 80277

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80278 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 80337

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80338 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 80397

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80398 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 80457

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80458 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 80517

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80518 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 80577

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db  80578 ATGTCCCCCTGA 80589


RESULT 5
AP000120
LOCUS       AP000120              100000 bp    DNA     linear   PRI 25-SEP-1999
DEFINITION  Homo sapiens genomic DNA of 21q22.1, GART and AML related,
            SLC5A3-f4A4 region, segment 3/8, complete sequence.
ACCESSION   AP000120
VERSION     AP000120.1  GI:4730889
```

```
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
  TITLE     Homo sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region
  JOURNAL   Published Only in DataBase (1999) In press
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1999) to the DDBJ/EMBL/GenBank databases. Mika
            Hirakawa, Japan Science and Technology Corporation (JST), Advanced
            Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
            Japan (E-mail:mika@tokyo.jst.go.jp,
            URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
            Fax:81-3-5214-8470)
COMMENT     This sequence is conducted by Kitasato University JST sequencing
            Laboratory as a JST sequencing team.
            Principal Investigator:Yoshiyuki Sakaki Ph.D.
            Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
            sakaki@hgc.ims.u-tokyo.ac.jp
            Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
            sequence is submitted by Human Genome Sequencing in ALIS project of
            JST.
            Japan Science and Technology Corporation (JST)
            5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081 Japan
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/) or send
            email to webmaster@www-alis.tokyo.jst.go.jp.
FEATURES              Location/Qualifiers
     source           1. .100000
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
     STS              32213. .32320
                      /standard_name="D21S1689"
                      /note="83F9aL-F/83F9aL-R;The location is between each
                      flanking site of PCR primers."
                      /db_xref="GDB:438410"
     STS              43934. .44157
                      /standard_name="D21S1920"
                      /note="AFMa086yf9;Genethon Marker;The location is between
                      each flanking site of PCR primers."
                      /db_xref="GDB:614718"
BASE COUNT    27731 a  21990 c  22220 g  28059 t
ORIGIN

  Query Match             100.0%;  Score 372;  DB 9;  Length 100000;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89520 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 89579

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89580 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 89639

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89640 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 89699

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89700 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 89759

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89760 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 89819

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89820 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 89879

Qy     361 ATGTCCCCCTGA 372
           ||||||||||||
Db   89880 ATGTCCCCCTGA 89891


RESULT 6
AP000167
LOCUS       AP000167              100000 bp    DNA     linear   PRI 08-JAN-2000
DEFINITION  Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region,
            clone B2344F14-f50E8, segment 3/9, complete sequence.
ACCESSION   AP000167
VERSION     AP000167.1  GI:4827132
KEYWORDS    HTG.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Homo sapiens 890,291bp genomic DNA of 21q22.1 (REGION: D21S226-AML
            CLONE RANGE: B2344F14-f50E8)
  JOURNAL   Published Only in DataBase (1999) In press
REFERENCE   2  (bases 1 to 100000)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-1999) to the DDBJ/EMBL/GenBank databases.
            Masahira Hattori, The Institute of Physical and Chemical Research
            (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
            Kitasato, Sagamihara, Kanagawa 228-8555, Japan
            (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-42-778-9923, Fax:81-42-778-9924)
COMMENT     E. coli transposon insertion:The present data does not contain E.
            coli transposon sequences which integrated in the
            original/previous sequences.  We determined the boundary between
            the insertion and genomic sequences experimentally, removed the
            insertion sequences, reconstituted the present data. The sequencing
            project is supported by Japan Science Technology Corporation (JST)
            and The Institute of Physical and Chemical Research (RIKEN).
FEATURES              Location/Qualifiers
     source           1. .100000
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="21"
                      /map="21q22.1"
BASE COUNT    27338 a  22306 c  22571 g  27785 t
ORIGIN

  Query Match             100.0%;  Score 372;  DB 9;  Length 100000;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72186 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 72245

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72246 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 72305

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   72306 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 72365

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db  72366 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 72425

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72426 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 72485

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  72486 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 72545

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db  72546 ATGTCCCCCTGA 72557


RESULT 7
AP001719
LOCUS       AP001719               340000 bp    DNA     linear   PRI 30-MAY-2000
DEFINITION  Homo sapiens genomic DNA, chromosome 21q, section 63/105.
ACCESSION   AP001719 AL163264 BA000005
VERSION     AP001719.1  GI:7768719
KEYWORDS    .
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
            Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
            Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
            Patterson,D., Reichwald,K., Rump,A., Schillhabel,M. and Schudy,A.
  TITLE     The DNA sequence of human chromosome 21. The chromosome 21 mapping
            and sequencing consortium
  JOURNAL   Nature 405 (6784), 311-319 (2000)
  MEDLINE   20289799
REFERENCE   2  (bases 1 to 340000)
  AUTHORS   Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
            Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
            Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
            Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
            Patterson,D., Reichwald,K., Rump,A., Schillhabel,M., Schudy,A.,
            Zimmermann,W., Rosenthal,A., Kudoh,J., Shibuya,K., Kawasaki,K.,
            Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
            Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordsiek,G.,
            Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
            Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
            Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
            Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
            Yaspo,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The
            Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic
            Sciences Center, Human Genome Research Group * Institute of
            Molecular Biotechnology, Genome Analysis * Keio University School
            of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome
            Analysis * Max-Planck Institute for Molecular Genetics (addresses
            see below)
COMMENT     On May 30, 2000 this sequence version replaced gi:7717333.
            The chromosome 21 mapping and sequencing consortium consisting of
            * RIKEN Genomic Sciences Center, Human Genome Research Group, *
            Sagamihara 228-8555, Japan,
            * e.mail: hattori@gsc.riken.go.jp
            * URL: http://hgp.gsc.riken.go.jp/
            and
            * Institute of Molecular Biotechnology, Genome Analysis, *
            Beutenbergstrasse 11, D-07745 Jena, Germany,
            * e.mail: gscj-submit@genome.imb-jena.de
            * URL: http://genome.imb-jena.de/
            and
            * Keio University School of Medicine, Molecular Biology, * Tokyo
            160-8582, Japan,
            * e.mail: nshimizu@dmb-med.keio.ac.jp
            * URL: http://www.dmb.med.keio.ac.jp/
            and
            * GBF, Dept. of Genome Analysis,
            * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
            info.genome@gbf.de
            * URL: http://genome.gbf.de/
            and
            * Max-Planck Institute for Molecular Genetics,
            * Ihnestrasse 73, D-14195 Berlin, Germany,
            * e.mail: info-chr21@molgen.mpg.de
            * URL: http://chr21.rz-berlin.mpg.de/
            AL163264: Submitted (10-Apr-2000).
FEATURES             Location/Qualifiers
     source          1. .340000
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
     source          <1. .29420
                     /note="Accession No. AP000467"
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="21"
                     /map="21q22.1"
                     /clone="R338L7, 5' partial"
                     /clone_lib="RPCI-11 BAC library"
     repeat_region   complement(1382. .1688)
                     /note="AluSp"
                     /rpt_family="SINE/Alu"
                     /rpt_type=DISPERSED
     repeat_region   complement(2099. .2390)
                     /note="AluSx"
                     /rpt_family="SINE/Alu"
                     /rpt_type=DISPERSED
     repeat_region   2799. .2884
                     /note="MIR"
                     /rpt_family="SINE/MIR"
                     /rpt_type=DISPERSED
     repeat_region   complement(2891. .3287)
                     /note="MER31A"
                     /rpt_family="LTR/MER4-group"
                     /rpt_type=DISPERSED
     repeat_region   3288. .3381
                     /note="MIR"
                     /rpt_family="SINE/MIR"
                     /rpt_type=DISPERSED
     misc_feature    4211. .5231
                     /note="CpG island"
     misc_feature    4272. .4279
                     /note="NotI site"
     repeat_region   4328. .4476
                     /note="(CGGGG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM
     mRNA            join(4392. .4740,12254. .35127)
                     /gene="SLC5A3"
                     /note="human solute carrier family 5, member 3, Accession
                     No. AF027153"
                     /product="Sodium/myo-inositol cotransporter"
     gene            4392. .35127
                     /gene="SLC5A3"
     exon            4392. .4740
                     /gene="SLC5A3"
                     /number=1
     misc_feature    4392. .4399
                     /gene="SLC5A3"
                     /note="NotI site"
     repeat_region   4810. .4985
                     /note="(CGGG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM
     repeat_region   5099. .5191
                     /note="(CCG)n"
                     /rpt_family="Simple_repeat"
```

```
                     /rpt_type=TANDEM
     repeat_region   10041. .10257
                     /note="MER58"
                     /rpt_family="DNA/MER1_type"
                     /rpt_type=DISPERSED
     repeat_region   10244. .10288
                     /note="MER58"
                     /rpt_family="DNA/MER1_type"
                     /rpt_type=DISPERSED
     repeat_region   complement(10381. .10677)
                     /note="AluSg"
                     /rpt_family="SINE/Alu"
                     /rpt_type=DISPERSED
     exon            12254. .35127
                     /gene="SLC5A3"
                     /number=2
     repeat_region   12578. .12623
                     /note="MIR"
                     /rpt_family="SINE/MIR"
                     /rpt_type=DISPERSED
     repeat_region   12891. .13088
                     /note="MER102"
                     /rpt_family="DNA/MER1_type"
                     /rpt_type=DISPERSED
     repeat_region   complement(15540. .15618)
                     /note="MIR"
                     /rpt_family="SINE/MIR"
                     /rpt_type=DISPERSED
     repeat_region   complement(15866. .16488)
                     /note="L1MC4"
                     /rpt_family="LINE/L1"
                     /rpt_type=DISPERSED
     repeat_region   complement(16480. .16548)
                     /note="L1MC5"
                     /rpt_family="LINE/L1"
                     /rpt_type=DISPERSED
     repeat_region   complement(16549. .16849)
                     /note="AluY"
                     /rpt_family="SINE/Alu"
                     /rpt_type=DISPERSED
     repeat_region   complement(16850. .17157)
                     /note="L1MC5"
                     /rpt_family="LINE/L1"
                     /rpt_type=DISPERSED
     repeat_region   17158. .17179
                     /note="(TTTTG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM
     repeat_region   17460. .17496
                     /note="(TG)n"
                     /rpt_family="Simple_repeat"
                     /rpt_type=TANDEM
     repeat_region   17576. .17723
                     /note="MIR"
                     /rpt_family="SINE/MIR"
                     /rpt_type=DISPERSED
     repeat_region   complement(18330. .18548)
                     /note="L2"
                     /rpt_family="LINE/L2"
                     /rpt_type=DISPERSED
     repeat_region   complement(18680. .18983)
                     /note="L2"
                     /rpt_family="LINE/L2"
                     /rpt_type=DISPERSED
     repeat_region   19578. .19789
                     /note="MIR"
                     /rpt_family="SINE/MIR"
                     /rpt_type=DISPERSED
     repeat_region   complement(19980. .20265)
                     /note="AluSx"
                     /rpt_family="SINE/Alu"

Query Match          100.0%;  Score 372;  DB 9;  Length 340000;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301427 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 301486

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301487 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 301546

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301547 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 301606

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301607 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 301666

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301667 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 301726

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301727 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 301786

Qy     361 ATGTCCCCCTGA 372
          ||||||||||||
Db  301787 ATGTCCCCCTGA 301798


RESULT 8
BC022699
LOCUS       BC022699               1664 bp    mRNA    linear   ROD 04-FEB-2002
DEFINITION  Mus musculus, RIKEN cDNA 2200002I16 gene, clone MGC:31447
            IMAGE:4481325, mRNA, complete cds.
ACCESSION   BC022699
VERSION     BC022699.1  GI:18490550
KEYWORDS    MGC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1664)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 44 Row: a Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis.
FEATURES             Location/Qualifiers
     source          1. .1664
                     /organism="Mus musculus"
```

```
                     /db_xref="LocusID:69143"
                     /db_xref="taxon:10090"
                     /clone="MGC:31447 IMAGE:4481325"
                     /tissue_type="Eye, retina, mouse strain C57Bl\6"
                     /clone_lib="NIH_MGC_94"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             90. .461
                     /codon_start=1
                     /product="RIKEN cDNA 2200002I16 gene"
                     /protein_id="AAH22699.1"
                     /db_xref="GI:18490551"
                     /translation="MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAE
                     NFYYVILYLMVMIGMFSFIVVAILVSTVKSKRREHSQHPYHQYIVEDWQEKYKSQILH
                     LEDSKATIHENMGATGFTVSP"
BASE COUNT      502 a    337 c    404 g    421 t
ORIGIN

  Query Match           72.0%;  Score 268;  DB 10;  Length 1664;
  Best Local Similarity  82.5%;  Pred. No. 2.4e-69;
  Matches  307;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | || ||| ||||||| || ||||| ||||| || | ||||  || ||||||||||
Db     90 ATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAAAAAGATTTTTATT 149

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          |||||||||||||  ||| |   |||||| ||||| ||| |  |||| ||||| |||| |
Db    150 ACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGCACTCCAGGCCAGA 209

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| ||||||||||||||| ||||||||||||||||||||||||| || ||||||
Db    210 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 269

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          || |||||| | |||||||||||||||||||| ||||| || ||| | || || ||||||
Db    270 TCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGAGAGCACTCC 329

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          |  |||| |||||||||||||| || || || ||||||||||||||||| || || |||
Db    330 CAGCACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTACAAAAGTCAGATC 389

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          || |||| ||||| || |||||||||||||||||||||||| || ||| | |||||||  |
Db    390 CTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACATGGGGGCGACGGGGTTCACA 449

Qy    361 ATGTCCCCCTGA 372
          |||| ||||||
Db    450 GTGTCACCCTGA 461


RESULT 9
AY050513
LOCUS       AY050513                372 bp    mRNA    linear   ROD 15-OCT-2001
DEFINITION  Cavia porcellus minK-related peptide 1 mRNA, complete cds.
ACCESSION   AY050513
VERSION     AY050513.1  GI:16151156
KEYWORDS    .
SOURCE      domestic guinea pig.
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Jiang,M., Zhang,M., Liu,J. and Tseng,G.-N.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-2001) Physiology, Virginia Commonwealth
            University, 1101 East Marshall Street, Richmond, VA 23298, USA
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Cavia porcellus"
                     /db_xref="taxon:10141"
                     /tissue_type="heart"
     CDS             1. .372
                     /note="Mirp1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAL13163.1"
                     /db_xref="GI:16151157"
                     /translation="MTTLANLTQTLEDAFKKVFITYMDSWRRNTTAEQQALQARVDAE
                     NFYYVILYLMVMIGMFAFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILH
                     LEDSKATIHENLGATGFTVSP"
BASE COUNT      95 a     98 c    105 g     74 t
ORIGIN

  Query Match           71.6%;  Score 266.4;  DB 10;  Length 372;
  Best Local Similarity  82.3%;  Pred. No. 5.2e-69;
  Matches  306;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | |||||| |||| || || ||||| ||||| || | ||||  || | |||| |||
Db      1 ATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAAAAGGTTTTCATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          |||||||||||||  ||| |   |||||||||||| || ||| |||| ||||| |||| |
Db     61 ACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCGCTCCAGGCCAGA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| ||||||||||||||| ||||||||||||||||||||||||| || ||||||
Db    121 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          | |||||| | |||||||||||||||||||| ||||| || ||| | ||||| ||||||
Db    181 GCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGGGAGCACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          | ||||| |||||||||||||| || ||||| |||||| | ||||| | ||| || |||
Db    241 CAGGACCCGTACCACCAGTACATCGTGGAGGATTGGCAGCAGAAGTATAGGAGTCAGATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||| |||| ||||| || |||||||||||||||||||||| | || ||| | ||||||| |
Db    301 TTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACCTGGGGGCGACGGGGTTCACA 360

Qy    361 ATGTCCCCCTGA 372
          |||| ||||||
Db    361 GTGTCACCCTGA 372


RESULT 10
AF071003
LOCUS       AF071003                468 bp    mRNA    linear   ROD 29-APR-1999
DEFINITION  Rattus norvegicus minK-related peptide 1 mRNA, complete cds.
ACCESSION   AF071003
VERSION     AF071003.1  GI:4704424
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Abbott,G.W., Sesti,F., Splawski,I., Buck,M.E., Lehmann,M.H.,
            Timothy,K.W., Keating,M.T. and Goldstein,S.A.
  TITLE     MiRP1 forms IKr potassium channels with HERG and is associated with
            cardiac arrhythmia
  JOURNAL   Cell 97 (2), 175-187 (1999)
  MEDLINE   99235979
REFERENCE   2  (bases 1 to 468)
  AUTHORS   Abbott,G.W., Sesti,F., Buck,M.E. and Goldstein,S.A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Section of Developmental Biology and
            Biophysics, Department of Pediatrics and Boyer Center for Molecular
            Medicine, Yale University School of Medicine, 295 Congress Avenue,
            New Haven, CT 06536, USA
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Rattus norvegicus"
```

```
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /sex="male"
                     /tissue_type="heart"
                     /dev_stage="10-12 weeks"
     CDS             35. .406
                     /note="potassium channel subunit; MiRP1"
                     /codon_start=1
                     /product="minK-related peptide 1"
                     /protein_id="AAD28087.1"
                     /db_xref="GI:4704425"
                     /translation="MTTLANLTQTLEDAFKKVFITYMDSWRRNTTAEQQALQARVDAE
                     NFYYVILYLMVMIGMFAFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILH
                     LEDSKATIHENLGATGFTVSP"
BASE COUNT      118 a    126 c    131 g     93 t
ORIGIN

  Query Match           71.6%;  Score 266.4;  DB 10;  Length 468;
  Best Local Similarity  82.3%;  Pred. No. 5.5e-69;
  Matches  306;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||| | |||||| |||| || || ||||| ||||| || | ||||  || | |||| |||
Db      35 ATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAAAAGGTTTTCATT 94

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  ||| |   |||||||||||| || ||| |||| ||||| |||| |
Db      95 ACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCGCTCCAGGCCAGA 154

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           || ||||| |||||||||||||| ||||||||||||||||||||||||| || ||||||
Db     155 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 214

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           | |||||| | |||||||||||||||||||| ||||| || ||| | ||||| ||||||
Db     215 GCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGGGAGCACTCC 274

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           | ||||| |||||||||||| || ||||| |||||| | ||||| | ||| || |||
Db     275 CAGGACCCGTACCACCAGTACATCGTGGAGGATTGGCAGCAGAAGTATAGGAGTCAGATC 334

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||| |||| ||||| || |||||||||||||||||||| | || ||| | ||||||| |
Db     335 TTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACCTGGGGGCGACGGGGTTCACA 394

Qy     361 ATGTCCCCCTGA 372
           |||| ||||||
Db     395 GTGTCACCCTGA 406


RESULT 11
AF329636
LOCUS       AF329636                 215 bp    mRNA    linear   MAM 28-SEP-2001
DEFINITION  Oryctolagus cuniculus K+/pacemaker channel beta subunit mirp1
            (kcne2) mRNA, partial cds.
ACCESSION   AF329636
VERSION     AF329636.1  GI:13194729
KEYWORDS    .
SOURCE      rabbit.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 215)
  AUTHORS   Yu,H., Wu,J., Potapova,I., Wymore,R.T., Holmes,B., Zuckerman,J.,
            Pan,Z., Wang,H., Shi,W., Robinson,R.B., El-Maghrabi,M.R.,
            Benjamin,W., Dixon,J., McKinnon,D., Cohen,I.S. and Wymore,R.S.
  TITLE     MinK-related peptide 1: A beta subunit for the HCN ion channel
            subunit family enhances expression and speeds activation
  JOURNAL   Circ. Res. 88 (12), E84-E87 (2001)
  MEDLINE   21313430
   PUBMED   11420311
REFERENCE   2  (bases 1 to 215)
  AUTHORS   Wymore,R.T., Holmes,B.A., Wymore,R.S., Yu,H., Wu,J., Potapova,I.,
            Zuckerman,J., Pan,Z., Wang,H., Shi,W., Robinson,R., El-Maghrabi,R.,
            Benjamin,W., Dixon,J.E., McKinnon,D. and Cohen,I.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-DEC-2000) Biology, The University of Tulsa, 600 S.
            College Av., Tulsa, OK 74104-3189, USA
FEATURES             Location/Qualifiers
     source          1. .215
                     /organism="Oryctolagus cuniculus"
                     /db_xref="taxon:9986"
     gene            <1. .>215
                     /gene="kcne2"
     CDS             <1. .>215
                     /gene="kcne2"
                     /codon_start=3
                     /product="K+/pacemaker channel beta subunit mirp1"
                     /protein_id="AAK15527.1"
                     /db_xref="GI:13194730"
                     /translation="AENFYYVILYLMVMIGMFSFIIVAILVSTVKSKRREHSNDPYHQ
                     YIVEDWQEKYKSQILHFEEAKATIHEN"
BASE COUNT       60 a     58 c     51 g     46 t
ORIGIN

  Query Match           50.1%;  Score 186.2;  DB 4;  Length 215;
  Best Local Similarity  91.6%;  Pred. No. 5.1e-45;
  Matches  197;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     125 ATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTCTT 184
           |||| |||||||||||||||||||||||| |||||||||||||||||||| ||||||| |
Db       1 ATGCGGAGAACTTCTACTATGTCATCCTCTACCTCATGGTGATGATTGGCATGTTCTCCT 60

Qy     185 TCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCCAATG 244
           |||||||||||||||||||||||||||| ||||| |||||||| |||||||||||||| |
Db      61 TCATCATCGTGGCCATCCTGGTGAGCACGGTGAAGTCCAAGAGGCGGGAACACTCCAACG 120

Qy     245 ACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATCTTGA 304
           |||||||||||||||||| || ||||||||||||||||||||||| ||||| || |||
Db     121 ACCCCTACCACCAGTACATCGTGGAGGACTGGCAGGAAAAGTACAAAAGCCAGATTTTGC 180

Qy     305 ATCTAGAAGAATCGAAGGCCACCATCCATGAGAAC 339
           || | |||||| | ||||||||||||||||||||
Db     181 ATTTCGAAGAAGCCAAGGCCACCATCCATGAGAAC 215


RESULT 12
AF387764
LOCUS       AF387764                 228 bp    mRNA    linear   MAM 08-NOV-2001
DEFINITION  Equus caballus minK related peptide 1-like mRNA, partial sequence.
ACCESSION   AF387764
VERSION     AF387764.1  GI:16797919
KEYWORDS    .
SOURCE      horse.
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 228)
  AUTHORS   Finley,M.R., Mitchell,R.E., Mitchell,B.M. and Freeman,L.C.
  TITLE     Post-translational modification of ERG in horse heart
  JOURNAL   FASEB J. 15, A1135 (2001)
REFERENCE   2  (bases 1 to 228)
  AUTHORS   Finley,M.R., Li,Y. and Freeman,L.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2001) Department of Anatomy and Physiology,
            Kansas State University, 1600 Denison Ave, Manhattan, KS 66506, USA
COMMENT     NCBI staff are still waiting for submitters to provide appropriate
            coding sequence information.
FEATURES             Location/Qualifiers
     source          1. .228
                     /organism="Equus caballus"
                     /db_xref="taxon:9796"
                     /tissue_type="atrium"
     misc_feature    44. .>228
                     /note="similar to minK related peptide 1; potassium
                     channel accessory protein; MiRP1; KCNE2"
```

```
BASE COUNT       68 a     57 c     51 g     51 t      1 others
ORIGIN

  Query Match             47.9%;  Score 178.2;  DB 4;  Length 228;
  Best Local Similarity   89.0%;  Pred. No. 1.3e-42;
  Matches  203;  Conservative    0;  Mismatches   24;  Indels    1;  Gaps    1;

Qy    124 GATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT-GATGATTGGAATGTTCTC 182
          ||||| ||||||||||||||| |||||| ||||||| ||||| ||||||||||||||||||
Db      1 GATGCGGAGAACTTCTACTACGTCATCTTGTACCTTATGGTAGATGATTGGAATGTTCTC 60

Qy    183 TTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCCAA 242
          ||||||||| || ||||||||||||||||| |||||||||||| |||| ||||||||||
Db     61 TTTCATCATTGTAGCCATCCTGGTGAGCACGGTGAAATCCAAGCGACGAGAACACTCCAA 120

Qy    243 TGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATCTT 302
          |||||||||||||||||| |||||||||||||| || || |||| ||| ||||| ||
Db    121 CGACCCCTACCACCAGTACATCGTAGAGGACTGGCAAGAGAAATACAGGAGTCAAATTTT 180

Qy    303 GAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGC 350
          |||||||| ||| | |||||||||||||||| ||| |||| |||||
Db    181 CAATCTAGAGGAACCAAAGGCCACCATCCATGANAACCTTGGCGCGGC 228


RESULT 13
RABIPCS
LOCUS       RABIPCS                 534 bp    DNA     linear   MAM 16-OCT-2001
DEFINITION  Oryctolagus cuniculus cardiac delayed rectifier potassium channel
            protein gene, complete cds.
ACCESSION   L41659
VERSION     L41659.1  GI:1246305
KEYWORDS    .
SOURCE      rabbit.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Salata,J.J., Jurkiewicz,N.K., Jow,B., Folander,K., Guinosso,P.J.
            Jr., Raynor,B., Swanson,R. and Fermini,B.
  TITLE     IK of rabbit ventricle is composed of two currents: evidence for
            IKs
  JOURNAL   Am. J. Physiol. 271 (6), H2477-H2489 (1996)
  MEDLINE   97151310
   PUBMED   8997308
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Oryctolagus cuniculus"
                     /strain="New Zealand White"
                     /db_xref="taxon:9986"
                     /clone="A1"
                     /clone_lib="Clontech genomic DNA library in EMBL3 SP6/T7"
                     /dev_stage="adult"
                     /note="breed: New Zealand White"
     CDS             133. .525
                     /function="cardiac potassium channel"
                     /note="Isk protein"
                     /codon_start=1
                     /product="cardiac delayed rectifier potassium channel
                     protein"
                     /protein_id="AAA93505.1"
                     /db_xref="GI:1246306"
                     /translation="MIPPNATAVMPFLTTLGEETAHLQGSSATSLARRGPLGDDGQME
                     ALYILMVLGFFGFFTLGIMLSYIRSQKLEHSHDPFNVYIEANDWQEKDRAYFQARVLE
                     SCRGCYVLENQLAVEHPDTHLPELKPSL"
BASE COUNT      105 a    175 c    149 g    105 t
ORIGIN

  Query Match             15.1%;  Score 56;  DB 4;  Length 534;
  Best Local Similarity   66.7%;  Pred. No. 6.6e-06;
  Matches   96;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    1;

Qy    151 CTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGC 210
          || ||| || |  || || | ||  | |||   ||| ||| | ||| |||| || |||||
Db    268 CTCTACATCCTCATGGTGCTCGGCTTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAGC 327

Qy    211 ACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAG-- 268
              |   ||| ||| || ||| |||||  ||||||||| | ||  ||||||||  |
Db    328 TACATCCGCTCCCAGAAACTGGAGCACTCGCATGACCCCTTCAACGTGTACATTGAGGCC 387

Qy    269 -AGGACTGGCAGGAAAAGTACAAG 291
           | ||||||||||| ||  ||| |
Db    388 AACGACTGGCAGGAGAAAGACAGG 411


RESULT 14
GPIISK
LOCUS       GPIISK                  750 bp    mRNA    linear   ROD 11-MAY-1994
DEFINITION  Cavia cobaya potassium channel mRNA, complete cds.
ACCESSION   L20462
VERSION     L20462.1  GI:484140
KEYWORDS    potassium channel.
SOURCE      Cavia cobaya adult cardiac muscle cDNA to mRNA.
  ORGANISM  Cavia porcellus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   Zhang,J., Jurkiewicz,N.K., Folander,K., Lazarides,E., Salata,J.J.
            and Swanson,R.
  TITLE     K+ currents expressed from the guinea pig cardiac IsK protein are
            enhanced by activators of protein kinase C
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91, 1766-1770 (1994)
  MEDLINE   94173910
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Cavia porcellus"
                     /db_xref="taxon:10141"
                     /cell_type="myocyte"
                     /tissue_type="cardiac muscle"
                     /dev_stage="adult"
     CDS             63. .440
                     /codon_start=1
                     /protein_id="AAA72394.1"
                     /db_xref="GI:484141"
                     /translation="MILPNSTAVMPFLTTVWQGTVQPSSNASGLARRSPLRDDGKLEA
                     LYILMVLGFFGFFTLGIMLSYIRSKKLEHSHDPFNVYIESDTWQEKDKAFFQARVLEN
                     CRSCCVIENQLTVEQPNTYLPEL"
BASE COUNT      189 a    199 c    174 g    188 t
ORIGIN

  Query Match             14.8%;  Score 55;  DB 10;  Length 750;
  Best Local Similarity   66.4%;  Pred. No. 1.4e-05;
  Matches   95;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    1;

Qy    151 CTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGC 210
          || ||| || |  || || | ||  | ||   |||| |||   ||| |||| || |||||
Db    195 CTCTACATCCTCATGGTGCTGGGCTTCTTTGGTTTCTTCACTCTGGGCATCATGCTGAGC 254

Qy    211 ACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---TA 267
            | |   |||||||| || ||| |||||  | ||||| | | ||  ||||||  |    |
Db    255 TATATTCGATCCAAGAAACTGGAGCACTCGCACGACCCGTTCAACGTGTACATCGAGTCA 314

Qy    268 GAGGACTGGCAGGAAAAGTACAA 290
          ||   ||||||||| ||| ||||
Db    315 GACACCTGGCAGGAGAAGGACAA 337


RESULT 15
AF135188
LOCUS       AF135188                390 bp    mRNA    linear   PRI 14-APR-1999
DEFINITION  Homo sapiens delayed rectifier potassium channel subunit IsK mRNA,
            complete cds.
ACCESSION   AF135188
VERSION     AF135188.1  GI:4583498
KEYWORDS    . .
SOURCE      human.
  ORGANISM  Homo sapiens
```

```
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 390)
  AUTHORS  Rae,J.L.
  TITLE    Delayed rectifier potassium channel subunit from human cornea
           epithelium
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 390)
  AUTHORS  Rae,J.L.
  TITLE    Direct Submission
  JOURNAL  Submitted (16-MAR-1999) Department of Physiology and Biophysics,
           Mayo Foundation, 200 1st Street SW, Rochester, MN 55905, USA
FEATURES             Location/Qualifiers
     source          1. .390
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="cornea epithelium"
     primer_bind     1. .17
     CDS             1. .390
                     /codon_start=1
                     /product="delayed rectifier potassium channel subunit IsK"
                     /protein_id="AAD25096.1"
                     /db_xref="GI:4583499"
                     /translation="MILSNTTAVTPFLTKLWQETVQQGGNMSGLARRSPRSSDGKLEA
                     LYVLMVLGFFGFFTLGIMLSYIRSKKLEHSNDPFNVYIESDAWQEKDKAYVQARVLES
                     YRSCYVVENHLAIEQPNTHLPETKPSP"
     primer_bind     complement(372. .390)
BASE COUNT       90 a    123 c    102 g     75 t
ORIGIN

  Query Match             14.3%;  Score 53.2;  DB 9;  Length 390;
  Best Local Similarity   63.6%;  Pred. No. 4.2e-05;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     132 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 191

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     192 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 251

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
            || | ||||| || ||| |||||  | |  ||
Db     252 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 285


Search completed: October 24, 2002, 13:54:33
Job time : 2063 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2002, 13:14:14 ; Search time 198 Seconds
(without alignments)
3225.718 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_445
Perfect score: 372
Sequence: 1 atgtctactttatccaatttt.....ggttcaaaatgtccccctga 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	372	100.0	372	22	AAI24432	Probe #14365 for g
	2	372	100.0	372	22	AAI09965	Probe #9956 used t
	3	372	100.0	372	22	AAS00245	Human potassium ch
	4	372	100.0	471	22	AAF80269	Nucleotide sequenc
	5	372	100.0	600	22	ABA09192	Human MiRP1 homolo
	6	372	100.0	600	22	AAK52645	Human polynucleoti
	7	372	100.0	655	22	AAK51661	Human polynucleoti
	8	372	100.0	732	21	AAC64071	Human potassium ch
	9	370.4	99.6	732	21	AAC64083	Human potassium ch
	10	370.4	99.6	732	21	AAC64084	Human potassium ch
	11	370.4	99.6	732	21	AAC64085	Human potassium ch
	12	370.4	99.6	732	21	AAC64086	Human potassium ch
	13	312	83.9	312	22	ABA49938	Human breast cell
	14	312	83.9	312	22	ABA67856	Human foetal liver
	15	312	83.9	312	22	ABA34913	Probe #13379 for g
	16	312	83.9	312	22	AAK16264	Human brain expres
	17	312	83.9	312	22	AAK42008	Human bone marrow
	18	312	83.9	312	22	AAI22773	Probe #12706 for g
	19	312	83.9	312	22	AAI48075	Probe #16761 used
	20	312	83.9	312	22	AAI08446	Probe #8437 used t
	21	295	79.3	450	22	ABA44797	Human breast cell
	22	295	79.3	450	22	ABA55252	Human foetal liver
	23	295	79.3	450	22	ABA24997	Probe #3463 for ge
	24	295	79.3	450	22	AAK03508	Human brain expres
	25	295	79.3	450	22	AAK28962	Human bone marrow
	26	295	79.3	450	22	AAI13549	Probe #3482 for ge
	27	295	79.3	450	22	AAI34911	Probe #3597 used t
	28	295	79.3	450	22	AAI03438	Probe #3429 used t
	29	266.4	71.6	372	22	AAS00246	Rat potassium chan
	30	266.4	71.6	468	21	AAC64072	Rat potassium chan
	31	233	62.6	471	22	AAI15256	Probe #5189 for ge
	32	233	62.6	471	22	AAI04990	Probe #4981 used t
c	33	53.2	14.3	231	22	ABA68478	Human foetal liver
c	34	53.2	14.3	231	22	ABA35463	Probe #13929 for g
c	35	53.2	14.3	231	22	AAK16847	Human brain expres
c	36	53.2	14.3	231	22	AAI23369	Probe #13302 for g
c	37	53.2	14.3	231	22	AAI48693	Probe #17379 used
c	38	53.2	14.3	390	22	ABA47286	Human breast cell
c	39	53.2	14.3	390	22	ABA65171	Human foetal liver
c	40	53.2	14.3	390	22	ABA32273	Probe #10739 for g
c	41	53.2	14.3	390	22	AAK13589	Human brain expres
c	42	53.2	14.3	390	22	AAK39329	Human bone marrow
c	43	53.2	14.3	390	22	AAI20142	Probe #10075 for g
c	44	53.2	14.3	390	22	AAI45342	Probe #14028 used
c	45	53.2	14.3	390	22	AAI05847	Probe #5838 used t

ALIGNMENTS

RESULT 1
AAI24432
ID AAI24432 standard; DNA; 372 BP.
XX
AC AAI24432;
XX
DT 12-OCT-2001 (first entry)
XX
DE Probe #14365 for gene expression analysis in human cervical cell sample.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 25; SEQ ID No 14365; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;

Query Match 100.0%; Score 372; DB 22; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-102;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    361 ATGTCCCCCTGA 372
```

RESULT 2
AAI09965
ID AAI09965 standard; DNA; 372 BP.
XX
AC AAI09965;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #9956 used to measure gene expression in human breast sample.
XX
KW Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
PT in a human breast -
XX
PS Claim 25; SEQ ID No 9956; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
CC staging, monitoring and prognosing diseases of the human breast,
CC particularly those diseases with polygenic aetiology. The diseases
CC include: breast cancer, disorders of development, inflammatory diseases
CC of the breast, fibrocystic changes, proliferative breast disease and
CC non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;

Query Match 100.0%; Score 372; DB 22; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-102;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    361 ATGTCCCCCTGA 372
```

RESULT 3
AAS00245
ID AAS00245 standard; DNA; 372 BP.

```
XX
AC   AAS00245;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Human potassium channel regulatory protein, Mink2, DNA sequence.
XX
KW   Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
KW   angina; asthma; diabetes; renal insufficiency; urinary incontinence;
KW   irritable colon; epilepsy; cerebrovascular ischaemia; autoimmune disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..372
FT                   /*tag= a
FT                   /product= "MINK2 potassium channel protein"
XX
PN   WO200114403-A1.
XX
PD   01-MAR-2001.
XX
PF   18-AUG-2000; 2000WO-US22799.
XX
PR   20-AUG-1999;   99US-0379201.
XX
PA   (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI   Ficker E,  Wible B,  Brown AM;
XX
DR   WPI; 2001-218424/22.
DR   P-PSDB; AAU00215.
XX
PT   Novel potassium channel gene termed MinK2 encoding potassium channel
PT   regulatory protein, useful for screening compounds that are useful for
PT   treating diseases caused by aberrant potassium activity -
XX
PS   Claim 1; Fig 9; 39pp; English.
XX
CC   The sequence represents the coding sequence of human potassium channel
CC   regulatory protein, Mink2. Mink2 sequence is useful for producing a
CC   potassium channel regulatory protein useful for in vitro or in vivo
CC   screening of agonistic or antagonistic compounds that are useful for
CC   treating diseases caused by aberrant potassium activity, such as human
CC   cardiac arrhythmias, hypertension, angina, asthma, diabetes, renal
CC   insufficiency, urinary incontinence, irritable colon, epilepsy,
CC   cerebrovascular ischaemia, and autoimmune disease.
XX
SQ   Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;

  Query Match           100.0%;  Score 372;  DB 22;  Length 372;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-102;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360

Qy     361 ATGTCCCCCTGA 372
           ||||||||||||
Db     361 ATGTCCCCCTGA 372


RESULT 4
AAF80269
ID   AAF80269 standard; DNA; 471 BP.
XX
AC   AAF80269;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Nucleotide sequence of human potassium channel subunit IsK2.
XX
KW   Human; potassium channel; IsK2; gene therapy; gastric motility;
KW   gastric acid secretion; anti-arrhythmic agent; myocardial infarction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             79..450
FT                   /*tag= a
FT                   /product= "potassium channel subunit IsK2"
XX
PN   WO200127246-A1.
XX
PD   19-APR-2001.
XX
PF   10-OCT-2000; 2000WO-US28014.
XX
PR   12-OCT-1999;   99US-0158781.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Swanson RJ,  Liu Y,  Folander K;
XX
DR   WPI; 2001-273764/28.
DR   P-PSDB; AAB67800.
XX
PT   New DNA encoding the IsK2 potassium channel subunit, useful e.g. for
PT   detecting mutations and screening for therapeutic agents  -
XX
PS   Claim 3; Fig 1A; 46pp; English.
XX
CC   The present sequence encodes a human potassium channel subunit,
CC   designated IsK2. The IsK2 polynucleotide, and derived probes, are
CC   used diagnostically to detect mutations in the IsK2 gene, to determine
CC   levels of mRNA expression and to isolate homologous sequences; for
CC   recombinant expression of IsK2; in gene therapy to increase potassium
CC   channel activity and to generate transgenic animals, as models and
CC   for drug screening. Recombinant IsK2 is used for studying biochemical
CC   activity of IsK2 and its role in disorders of gastric motility and
CC   gastric acid secretion, and to raise specific antibodies. IsK2
CC   modulators are potentially useful for treating diseases associated with
CC   increased or reduced potassium channel activity, e.g. as
CC   anti-arrhythmic agents for treating myocardial infarction and as
CC   regulators of gastric acid secretion.
XX
SQ   Sequence 471 BP; 143 A; 110 C; 103 G; 115 T; 0 other;

  Query Match           100.0%;  Score 372;  DB 22;  Length 471;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-102;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 138
```

```
Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 198

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     199 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 258

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     259 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 318

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 378

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     379 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 438

Qy     361 ATGTCCCCCTGA 372
           ||||||||||||
Db     439 ATGTCCCCCTGA 450
```

RESULT 5
ABA09192
ID ABA09192 standard; cDNA; 600 BP.
XX
AC ABA09192;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human MiRP1 homologue-encoding cDNA, SEQ ID NO:968.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11948.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 826; 1963pp; English.

XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other;

  Query Match   100.0%; Score 372; DB 22; Length 600;
  Best Local Similarity   100.0%; Pred. No. 2e-102;
  Matches 372; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 97

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 157

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 217

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 277

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 337

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 397

Qy     361 ATGTCCCCCTGA 372
           ||||||||||||
Db     398 ATGTCCCCCTGA 409
```

```
RESULT 6
AAK52645
ID   AAK52645 standard; cDNA; 600 BP.
XX
AC   AAK52645;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 2174.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79512.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 4539-4540; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other;

  Query Match            100.0%;  Score 372;  DB 22;  Length 600;
  Best Local Similarity  100.0%;  Pred. No. 2e-102;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 97

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 157

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 217

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 277

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 337

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 397

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    398 ATGTCCCCCTGA 409


RESULT 7
AAK51661
ID   AAK51661 standard; cDNA; 655 BP.
XX
AC   AAK51661;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 206.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US04098.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
PR   20-JUN-2000; 2000US-0598075.
PR   19-JUL-2000; 2000US-0620325.
PR   01-SEP-2000; 2000US-0654936.
PR   15-SEP-2000; 2000US-0663561.
PR   20-OCT-2000; 2000US-0693325.
PR   30-NOV-2000; 2000US-0728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y,  Ma Y;
PI   Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM78528.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities,
PT   useful in diagnosis and gene therapy -
XX
PS   Claim 1; Page 1024; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
```

```
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC   (AAM80020) are omitted as the relevant pages from the sequence listing
CC   were missing at the time of publication.
XX
SQ   Sequence 655 BP; 196 A; 154 C; 146 G; 153 T; 6 other;

  Query Match            100.0%;  Score 372;  DB 22;  Length 655;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-102;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     93 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 152

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    153 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 212

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    213 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 272

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    273 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 332

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 392

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 452

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    453 ATGTCCCCCTGA 464


RESULT 8
AAC64071
ID   AAC64071 standard; cDNA; 732 BP.
XX
AC   AAC64071;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) cDNA, SEQ ID NO:1.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; ss.
XX
OS   Homo sapiens.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29585.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 1; Page 118-119; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents cDNA encoding human KCNE2 (MiRP1).
XX
SQ   Sequence 732 BP; 221 A; 152 C; 157 G; 202 T; 0 other;

  Query Match            100.0%;  Score 372;  DB 21;  Length 732;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-102;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    434 ATGTCCCCCTGA 445


RESULT 9
AAC64083
ID   AAC64083 standard; DNA; 732 BP.
```

```
XX
AC   AAC64083;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) Q9E mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29593.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 151 C; 158 G; 202 T; 0 other;

  Query Match            99.6%;  Score 370.4;  DB 21;  Length 732;
  Best Local Similarity  99.7%;  Pred. No. 6.7e-102;
  Matches  371;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACAGAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCCTGA 372
           ||||||||||||
Db     434 ATGTCCCCCTGA 445


RESULT 10
AAC64084
ID   AAC64084 standard; DNA; 732 BP.
XX
AC   AAC64084;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) M54T mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29594.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
```

```
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

  Query Match             99.6%;  Score 370.4;  DB 21;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 6.7e-102;
  Matches  371;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCACGGTGATGATTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy     301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy     361 ATGTCCCCCTGA 372
          ||||||||||||
Db     434 ATGTCCCCCTGA 445


RESULT 11
AAC64085
ID   AAC64085 standard; DNA; 732 BP.
XX
AC   AAC64085;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) I57T mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29595.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;

  Query Match             99.6%;  Score 370.4;  DB 21;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 6.7e-102;
  Matches  371;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGACTGGAATGTTC 253

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    434 ATGTCCCCCTGA 445


RESULT 12
AAC64086
ID   AAC64086 standard; DNA; 732 BP.
XX
AC   AAC64086;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human potassium channel protein KCNE2 (MiRP1) T8A mutant DNA.
XX
KW   Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
KW   MinK-related; long QT syndrome; cardiac arrhythmia;
KW   drug screening; knockout mouse; transgenic animal; ion channel disorder;
KW   fast delayed rectifier potassium channel; anti-KNCE2 antibody;
KW   HERG; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200063434-A1.
XX
PD   26-OCT-2000.
XX
PF   14-APR-2000; 2000WO-US10004.
XX
PR   15-APR-1999;   99US-0129404.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (UYYA ) UNIV YALE.
XX
PI   Abbott GW,  Sesti F,  Splawski I,  Keating MT,  Goldstein SAN;
XX
DR   WPI; 2000-672747/65.
DR   P-PSDB; AAB29596.
XX
PT   Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for
PT   diagnosing and treating ion channel disorders, especially long QT
PT   syndrome -
XX
PS   Claim 56; Page -; 132pp; English.
XX
CC   The invention relates to novel ion channel proteins related to
CC   KNCE1 (MinK) and to nucleic acids encoding them. The proteins of
CC   the invention are human and rat KCNE2 (MiRP1; AAB29585 and AAB29586,
CC   respectively); human and mouse KCNE3 (MiRP2; AAB29587 and AAB29588,
CC   respectively); and human and mouse KCNE4 (MiRP3; AAB29589 and AAB29590,
CC   respectively). The cDNAs encoding these proteins are given in AAC64071-
CC   AAC64076. KCNE2, along with HERG, forms cardiac fast delayed rectifier
CC   potassium channels (I-KR), mutations in which are associated with long
CC   QT syndrome. The invention also relates to methods of diagnosing long QT
CC   syndrome using the KCNE2, KCNE3 or KCNE4 genes, a knockout mouse with a
CC   disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic
CC   nonhuman animals comprising a heterologous ion channel protein gene
CC   of the invention, a transgenic animal comprising human KNCE2 and HERG
CC   DNA, and methods of and screening drugs for treating long QT syndrome
CC   using KCNE2 proteins (including mutants), nucleic acids encoding them
CC   and antibodies against KNCE2 proteins. The methods, antibodies, nucleic
CC   acids, and proteins may be used for diagnosing or treating ion channel
CC   disorders, especially long QT syndrome. Transgenic animals comprising
CC   KCNE2 and HERG are useful for testing anti-long QT syndrome drugs.
CC   The present sequence represents DNA encoding a mutant human KCNE2
CC   (MiRP1) specifically claimed for use in diagnostic and drug screening
CC   methods of the invention.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type human KNCE2 cDNA sequence shown on page
CC   118-119.
XX
SQ   Sequence 732 BP; 220 A; 152 C; 158 G; 202 T; 0 other;

  Query Match             99.6%;  Score 370.4;  DB 21;  Length 732;
  Best Local Similarity   99.7%;  Pred. No. 6.7e-102;
  Matches  371;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     74 ATGTCTACTTTATCCAATTTCGCACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 133

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 193

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 253

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 313

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    314 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 373

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 433

Qy    361 ATGTCCCCCTGA 372
          ||||||||||||
Db    434 ATGTCCCCCTGA 445


RESULT 13
ABA49938
ID   ABA49938 standard; DNA; 312 BP.
XX
AC   ABA49938;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human breast cell single exon nucleic acid probe #8633.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00662.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
```

```
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes  -
XX
PS   Claim 4; SEQ ID NO 8633; 327pp + sequence listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a single exon nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;

  Query Match             83.9%;  Score 312;  DB 22;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 2e-84;
  Matches  312;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      54 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 60

Qy     114 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120

Qy     174 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 180

Qy     234 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 240

Qy     294 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 300

Qy     354 GTTCAAAATGTC 365
           ||||||||||||
Db     301 GTTCAAAATGTC 312


RESULT 14
ABA67856
ID   ABA67856 standard; DNA; 312 BP.
XX
AC   ABA67856;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #16161.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 4; SEQ ID NO 16161; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;

  Query Match             83.9%;  Score 312;  DB 22;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 2e-84;
  Matches  312;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      54 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 60

Qy     114 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120

Qy     174 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 180

Qy     234 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 240

Qy     294 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 300

Qy     354 GTTCAAAATGTC 365
           ||||||||||||
Db     301 GTTCAAAATGTC 312


RESULT 15
ABA34913
ID   ABA34913 standard; DNA; 312 BP.
XX
AC   ABA34913;
XX
DT   23-JAN-2002  (first entry)
XX
```

```
DE   Probe #13379 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 13379; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;

  Query Match             83.9%;  Score 312;  DB 22;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 2e-84;
  Matches  312;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      54 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 60

Qy     114 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 173
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120

Qy     174 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 233
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGA 180

Qy     234 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 293
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAG 240

Qy     294 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 353
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGG 300

Qy     354 GTTCAAAATGTC 365
           ||||||||||||
Db     301 GTTCAAAATGTC 312


Search completed: October 24, 2002, 13:19:51
Job time : 201 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2002, 13:16:15 ; Search time 43 Seconds
(without alignments)
2125.015 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_445
Perfect score: 372
Sequence: 1 atgtctactttatccaatttt.....ggttcaaaatgtccccctga 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	53.2	14.3	398	1	US-08-118-101A-5	Sequence 5, Appli
	2	53.2	14.3	1703	3	US-09-135-021-77	Sequence 77, Appl
	3	53.2	14.3	1703	4	US-09-135-020-3	Sequence 3, Appli
	4	53.2	14.3	1703	4	US-09-135-010A-3	Sequence 3, Appli
	5	36.6	9.8	2652	1	US-08-318-831-1	Sequence 1, Appli
	6	36	9.7	1380	1	US-08-110-286A-1	Sequence 1, Appli
	7	33.6	9.0	645	3	US-09-069-896-2	Sequence 2, Appli
	8	33	8.9	606	4	US-09-328-111-133	Sequence 133, App
c	9	33	8.9	2912	4	US-09-307-143-3	Sequence 3, Appli
c	10	32.4	8.7	837	4	US-08-998-416-303	Sequence 303, App
	11	30.6	8.2	6822	4	US-09-426-998-3	Sequence 3, Appli
	12	30.6	8.2	7741	4	US-09-426-998-4	Sequence 4, Appli
c	13	29.8	8.0	2266	2	US-08-724-394A-18	Sequence 18, Appl
	14	29.8	8.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
	15	29.8	8.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
	16	29.8	8.0	246240	2	US-08-724-394A-22	Sequence 22, Appl
	17	29.6	8.0	462	3	US-08-863-813A-33	Sequence 33, Appl
	18	29.6	8.0	3273	6	5516630-1	Patent No. 5516630
	19	29.6	8.0	7486	3	US-08-475-886-5	Sequence 5, Appli
	20	29.6	8.0	7486	4	US-08-397-232-3	Sequence 3, Appli
	21	29.6	8.0	7488	3	US-08-475-886-3	Sequence 3, Appli
	22	29.6	8.0	7493	3	US-08-475-886-1	Sequence 1, Appli
	23	29.6	8.0	7493	4	US-08-397-232-1	Sequence 1, Appli
	24	29.6	8.0	7493	4	US-09-171-387-1	Sequence 1, Appli
	25	29.4	7.9	3947	4	US-08-975-762-47	Sequence 47, Appl
	26	29.4	7.9	3947	4	US-09-295-028-47	Sequence 47, Appl
	27	29.4	7.9	3947	4	US-09-106-582-47	Sequence 47, Appl
c	28	29.2	7.8	352	4	US-09-439-313-421	Sequence 421, App
c	29	29.2	7.8	630	4	US-08-646-695-13	Sequence 13, Appl
	30	29.2	7.8	630	4	US-08-646-695-14	Sequence 14, Appl
c	31	29.2	7.8	630	5	PCT-US96-06053-13	Sequence 13, Appl
	32	29.2	7.8	630	5	PCT-US96-06053-14	Sequence 14, Appl
c	33	29.2	7.8	2380	1	US-08-572-951-3	Sequence 3, Appli
c	34	29.2	7.8	14311	4	US-08-646-695-1	Sequence 1, Appli
	35	29.2	7.8	14311	4	US-08-646-695-7	Sequence 7, Appli
c	36	29.2	7.8	14311	5	PCT-US96-06053-1	Sequence 1, Appli
	37	29.2	7.8	14311	5	PCT-US96-06053-7	Sequence 7, Appli
c	38	29	7.8	744	3	US-08-969-644-17	Sequence 17, Appl
c	39	29	7.8	744	3	US-08-444-189-17	Sequence 17, Appl
c	40	29	7.8	744	4	US-08-468-544-17	Sequence 17, Appl
	41	29	7.8	1983	1	US-08-073-799C-9	Sequence 9, Appli
c	42	29	7.8	7502	3	US-08-969-644-6	Sequence 6, Appli
c	43	29	7.8	7502	3	US-08-444-189-6	Sequence 6, Appli
c	44	29	7.8	7502	4	US-08-468-544-6	Sequence 6, Appli
	45	28.8	7.7	2168	2	US-08-633-879C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-118-101A-5
; Sequence 5, Application US/08118101A
; Patent No. 5620892
; GENERAL INFORMATION:
; APPLICANT: Kurtz, Stephen E.
; APPLICANT: Knickerbocker, Aron M.
; APPLICANT: McCullough, John R.
; TITLE OF INVENTION: A STRAIN OF SACCHAROMYCES CEREVISIAE
; TITLE OF INVENTION: EXPRESSING THE GENE ENCODING POTASSIUM TRANSPORTER MINK
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,101A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..398
US-08-118-101A-5

Query Match 14.3%; Score 53.2; DB 1; Length 398;
Best Local Similarity 63.6%; Pred. No. 1.3e-08;
Matches 98; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

```
Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    141 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 200

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    201 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 260

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          || | |||||| || ||| |||||  | |  ||
Db    261 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 294


RESULT 2
US-09-135-021-77
; Sequence 77, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-021-77

  Query Match             14.3%;  Score 53.2;  DB 3;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 3
US-09-135-020-3
; Sequence 3, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/135,020
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-020-3

  Query Match             14.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 4
US-09-135-010A-3
; Sequence 3, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
;  APPLICANT:  Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION:  KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE:  2323-133
;  CURRENT APPLICATION NUMBER: US/09/135,010A
;  CURRENT FILING DATE:  1998-08-17
;  PRIOR APPLICATION NUMBER:  60/094,477
;  PRIOR FILING DATE:  1998-07-29
;  PRIOR APPLICATION NUMBER:  08/921,068
;  PRIOR FILING DATE:  1997-08-29
;  PRIOR APPLICATION NUMBER:  08/739,383
;  PRIOR FILING DATE:  1996-10-29
;  PRIOR APPLICATION NUMBER:  60/019,014
;  PRIOR FILING DATE:  1995-12-22
;  NUMBER OF SEQ ID NOS:  116
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-010A-3

  Query Match             14.3%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;
```

```
Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   |||||
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 5
US-08-318-831-1
; Sequence 1, Application US/08318831
; Patent No. 5656595
;  GENERAL INFORMATION:
;    APPLICANT:  Schweighoffer, Fabien
;    APPLICANT:  Tocque, Bruno
;    TITLE OF INVENTION:  PEPTIDES HAVING A GDP EXCHANGE FACTOR
;    TITLE OF INVENTION:  ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES,
;    TITLE OF INVENTION:  PREPARATION AND UTILIZATION
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.1 (EPO Patentin)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,831
;      FILING DATE:  19 October 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR92/04827
;      FILING DATE:  21-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, Julie K.
;      REGISTRATION NUMBER:  P-38,619
;      REFERENCE/DOCKET NUMBER:  ST92033-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2652 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2445
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  445..2445 (SEQ ID NO 3)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  976..2445 (SEQ ID NO 4)
US-08-318-831-1

  Query Match             9.8%;  Score 36.6;  DB 1;  Length 2652;
  Best Local Similarity   53.1%;  Pred. No. 0.018;
  Matches   78;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;
```

```
Qy     55 TTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAA 114
          | ||  | |  | |   | | | |  ||| ||| |  || ||||    | | ||  || |
Db   2402 TCTACGAGTCTTCTCTCCGAATAGAACCAAAACTCCCCACCTGAAGCTGTGCCCAGCCCA 2461

Qy    115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
          | |  || || | | | | | || | | |||  | || ||||||  |  | ||   | ||
Db   2462 GACCCAGCTGCTCCCGGGGACATGTGCTAGATGATACTGTACATATTCGTTTGGTTTCAC 2521

Qy    175 ATGTTCTCTTTCATCATCGTGGCCATC 201
            | | |  ||| |||   ||  | ||
Db   2522 TGGATTTTCTTCTTCAGTATGTGCTTC 2548


RESULT 6
US-08-110-286A-1
; Sequence 1, Application US/08110286A
; Patent No. 5728545
;  GENERAL INFORMATION:
;    APPLICANT:  Perrin, Marilyn H.
;    APPLICANT:  Chen, Ruoping
;    APPLICANT:  Lewis, Kathy A.
;    APPLICANT:  Vale Jr., Wylie W.
;    APPLICANT:  Donaldson, Cynthia J.
;    TITLE OF INVENTION:  CLONING AND RECOMBINANT PRODUCTION OF
;    TITLE OF INVENTION:  CRF RECEPTOR(S)
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pretty, Schroeder, Brueggemann & Clark
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/110,286A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/079,320
;      FILING DATE:  18-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P41 9439
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-546-4737
;      TELEFAX:  619-546-9392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1380 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  82..1329
;      OTHER INFORMATION:  /product= "HUMAN PITUITARY
;      OTHER INFORMATION:  CRF-RECEPTOR"
;      OTHER INFORMATION:  /note= "This sequence is encoded by clone
;      OTHER INFORMATION:  "CRF-R1"."
US-08-110-286A-1

  Query Match             9.7%;  Score 36;  DB 1;  Length 1380;
  Best Local Similarity   52.7%;  Pred. No. 0.019;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;
```

```
Qy     115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     862 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 921

Qy     175 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 234
             || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db     922 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 981

Qy     235 CACTCCAATGACCCCTACCACCAGTACA 262
             | |||           |   |||||||
Db     982 TCCACCACGTCTGAGACCATTCAGTACA 1009


RESULT 7
US-09-069-896-2
; Sequence 2, Application US/09069896
; Patent No. 6071720
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Patterson, Chandra
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DELAYED RECTIFIER POTASSIUM
;    TITLE OF INVENTION:  CHANNEL HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,896
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0507 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  645 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  BRSTNOT03
;      CLONE:  637471
US-09-069-896-2

  Query Match             9.0%;  Score 33.6;  DB 3;  Length 645;
  Best Local Similarity   53.9%;  Pred. No. 0.081;
  Matches   69;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           | | ||| |  ||||  | ||     | | |    |  || |  | |  ||| || || |
Db     200 CTTCTACATTCTGGTTGTCATGTCCTTCTACGGCATTTTCTTGATCGGAATCATGCTGGG 259

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGA 269
           |    |||||||||||||| |||||  |         || |   |  | |||||  |  ||
Db     260 CTACATGAAATCCAAGAGGCGGGAGAAGAAGTCCAGCCTCCTGCTGCTGTACAAAGACGA 319

Qy     270 GGACTGGC 277
           |||  |||
Db     320 GGAGCGGC 327


RESULT 8
US-09-328-111-133
; Sequence 133, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
;   LENGTH: 606
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(606)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-133

  Query Match             8.9%;  Score 33;  DB 4;  Length 606;
  Best Local Similarity   58.8%;  Pred. No. 0.13;
  Matches   57;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy     135 CTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGT 194
           |||||  || |||| |||| | | |||    | || || |      |||| | |||   || |
Db     124 CTTCTTCTTTGTCTTCCTTTTCTTCAGCCTCATCATCGCTTACTTCTTTATCACGTTCCT 183

Qy     195 GGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGG 231
           |  |     ||| | || || |||||| | || |
Db     184 TCTCCACAAAAAGAGTAATGGGATATCCAATAAACTG 220


RESULT 9
US-09-307-143-3/c
; Sequence 3, Application US/09307143
; Patent No. 6335157
; GENERAL INFORMATION:
;  APPLICANT: Gonzalez c.
;  APPLICANT: Lange, B.
;  TITLE OF INVENTION: METHODS BASED ON LOCALIZATION OF HSP90 TO THE
;  TITLE OF INVENTION: CENTROSOME
;  FILE REFERENCE: 9882-003
;  CURRENT APPLICATION NUMBER: US/09/307,143
;  CURRENT FILING DATE: 1999-05-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2912
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(2256)
US-09-307-143-3

  Query Match             8.9%;  Score 33;  DB 4;  Length 2912;
  Best Local Similarity   58.8%;  Pred. No. 0.31;
  Matches   57;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy    135 CTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGT 194
          ||||| || |||| |||| | | |||   | || || |     |||| | |||   || |
Db    790 CTTCTTCTTTGTCTTCCTTTTCTTCAGCCTCATCATCGCTTACTTCTTTATCACGTTCCT 731

Qy    195 GGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGG 231
          |  |     ||| | || || |||||| | || |
Db    730 TCTCCACAAAAAGAGTAATGGGATATCCAATAAACTG 694


RESULT 10
US-08-998-416-303/c
; Sequence 303, Application US/08998416
; Patent No. 6239264
;  GENERAL INFORMATION:
;    APPLICANT:  Philippsen, Peter
;    APPLICANT:  Pohlmann, Rainer
;    APPLICANT:  Steiner, Sabine
;    APPLICANT:  Mohr, Christine
;    APPLICANT:  Wendland, Jurgen
;    APPLICANT:  Knechtle, Philipp
;    APPLICANT:  Rebischung, Corinne
;    TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1152
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6239264artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  No. 6239264th Carolina
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/998,416
;      FILING DATE:  24-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  CH 0016/97
;      FILING DATE:  31-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  303:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  837 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  PAG1249RP
US-08-998-416-303

  Query Match             8.7%;  Score 32.4;  DB 4;  Length 837;
  Best Local Similarity   50.0%;  Pred. No. 0.24;
  Matches   81;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy    166 ATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAG 225
          || | | | |||   ||  |||  |    | ||| |||   |  |  |     ||
Db    452 ATCAGTAGCATGACATCGCTCACGACTACAGACATACTGCACACAGCCAAGGCTCTTAAC 393

Qy    226 AGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAG 285
          | || |  | | | ||| | ||   ||  |  |||| |    ||||||  || |  || |
Db    392 ATACTGCGATATTACAAGGGCCAGCACATCTTGTACCTGAACGAGGACGTGCTGCTAAGG 333

Qy    286 TACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACC 327
          ||| |||  |  ||  |||   |    |||||  | | ||
Db    332 TACGAGAAGCTGATAGCGAAGAAAAGGCGATCGATCGACCCC 291


RESULT 11
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
;  APPLICANT: DUBIN, ADRIENNE E.
;  APPLICANT:  PYATI, JAYASHREE
;  APPLICANT:  ZHU, JESSICA Y
;  APPLICANT:  ERLANDER, MARK G
;  APPLICANT:  GALINDO, JOSE E
;  TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
;  TITLE OF INVENTION:  CHANNEL (ALPHA1G-C)
;  FILE REFERENCE: ORT-1057
;  CURRENT APPLICATION NUMBER: US/09/426,998
;  CURRENT FILING DATE:  1999-10-26
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
;   LENGTH: 6822
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-426-998-3

  Query Match             8.2%;  Score 30.6;  DB 4;  Length 6822;
  Best Local Similarity   58.1%;  Pred. No. 3.4;
  Matches   54;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy    122 TTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCT 181
          | |||||| |   ||||||| || |||||   | | || |  | || || |     | ||
Db   1091 TGGATGCTCATTCCTTCTACAATTTCATCTACTTCATCCTCCTCATCATCGTGGGCTCCT 1150

Qy    182 CTTTCATCATCGTGGCCATCCTGGTGAGCACTG 214
            ||||| |||        |||||||   | ||
Db   1151 TCTTCATGATCAACCTGTGCCTGGTGGTGATTG 1183


RESULT 12
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
;  APPLICANT: DUBIN, ADRIENNE E.
;  APPLICANT:  PYATI, JAYASHREE
;  APPLICANT:  ZHU, JESSICA Y
;  APPLICANT:  ERLANDER, MARK G
;  APPLICANT:  GALINDO, JOSE E
;  TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
;  TITLE OF INVENTION:  CHANNEL (ALPHA1G-C)
;  FILE REFERENCE: ORT-1057
;  CURRENT APPLICATION NUMBER: US/09/426,998
;  CURRENT FILING DATE:  1999-10-26
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
;   LENGTH: 7741
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-426-998-4
```

```
  Query Match             8.2%;  Score 30.6;  DB 4;  Length 7741;
  Best Local Similarity   58.1%;  Pred. No. 3.6;
  Matches   54;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy     122 TTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCT 181
           | |||||| |   ||||||| || |||||   | | || |  | || || |     | ||
Db    1613 TGGATGCTCATTCCTTCTACAATTTCATCTACTTCATCCTCCTCATCATCGTGGGCTCCT 1672

Qy     182 CTTTCATCATCGTGGCCATCCTGGTGAGCACTG 214
           ||||| |||        |||||||   | ||
Db    1673 TCTTCATGATCAACCTGTGCCTGGTGGTGATTG 1705


RESULT 13
US-08-724-394A-18/c
; Sequence 18, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2266 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..2266
;      OTHER INFORMATION:  /note= "cDNA 22B"
US-08-724-394A-18

  Query Match             8.0%;  Score 29.8;  DB 2;  Length 2266;
  Best Local Similarity   60.5%;  Pred. No. 3.3;
  Matches   49;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy     152 TGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCA 211
           ||| |  ||||| |||||| | |||| ||    |||    |   |  ||| ||||||
Db     560 TGTTCACCATGGCGATGATCGCAATGCTCAGACTCACACGCTGCGTTATCATGGTGAAGT 501

Qy     212 CTGTGAAATCCAAGAGACGGG 232
           || ||| | || || | | |
Db     500 TTGAGAAGTGCATGATAAGAG 480


RESULT 14
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-20

  Query Match             8.0%;  Score 29.8;  DB 2;  Length 246240;
  Best Local Similarity   60.5%;  Pred. No. 50;
  Matches   49;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy     152 TGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCA 211
           ||| |  ||||| |||||| | |||| ||    |||    |   |  ||| ||||||
Db   29016 TGTTCACCATGGCGATGATCGCAATGCTCAGACTCACACGCTGCGTTATCATGGTGAAGT 29075

Qy     212 CTGTGAAATCCAAGAGACGGG 232
           || ||| | || || | | |
Db   29076 TTGAGAAGTGCATGATAAGAG 29096


RESULT 15
US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-21

  Query Match             8.0%;  Score 29.8;  DB 2;  Length 246240;
  Best Local Similarity   60.5%;  Pred. No. 50;
  Matches   49;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy    152 TGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCA 211
          ||| |  ||||| |||||| | |||| ||    |||    |   |  ||| ||||||
Db  29016 TGTTCACCATGGCGATGATCGCAATGCTCAGACTCACACGCTGCGTTATCATGGTGAAGT 29075

Qy    212 CTGTGAAATCCAAGAGACGGG 232
          || ||| | || || | | |
Db  29076 TTGAGAAGTGCATGATAAGAG 29096


Search completed: October 24, 2002, 14:20:05
Job time : 147 secs
```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 24, 2002, 13:15:40 ; Search time 1605 Seconds
(without alignments)
3128.266 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_445
Perfect score: 372
Sequence: 1 atgtctactttatccaatttt.....ggttcaaaatgtccccctga 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	357.8	96.2	803	10	BG208163	BG208163 RST27654
	2	336	90.3	410	9	AI962650	AI962650 wq42e03.x
	3	336	90.3	429	9	AI654552	AI654552 wb48b12.x
	4	331.8	89.2	391	9	AI339609	AI339609 qq42a07.x
	5	328	88.2	372	9	AI246239	AI246239 qi29g04.x
	6	269.6	72.5	1691	11	AK008619	AK008619 Mus muscu
	7	260.8	70.1	470	10	D85797	D85797 D85797 Rat
	8	245	65.9	1003	10	BG261965	BG261965 602373784
	9	177.8	47.8	746	10	BG221966	BG221966 RST41783
	10	168.2	45.2	351	10	BG938225	BG938225 1Abo14A12
	11	160	43.0	188	9	AA633404	AA633404 np69h11.s
	12	119.4	32.1	121	9	AA935321	AA935321 oo71g09.s
c	13	99	26.6	311	9	AW869303	AW869303 MR3-SN006
	14	90	24.2	314	9	BB564873	BB564873 BB564873
	15	57.6	15.5	272	9	BB574249	BB574249 BB574249
	16	57.2	15.4	358	10	BE486735	BE486735 174950 BA
	17	53.2	14.3	716	10	BI459541	BI459541 603200548
	18	52.8	14.2	464	9	AA667912	AA667912 vv19f07.r
	19	52.8	14.2	603	9	AI956381	AI956381 ul74e07.y
	20	52.8	14.2	674	9	BB613272	BB613272 BB613272
	21	52.8	14.2	754	11	AK008938	AK008938 Mus muscu
	22	51.8	13.9	311	9	AW869303	AW869303 MR3-SN006
c	23	51	13.7	424	10	BM389584	BM389584 UI-R-CN1-
	24	50.8	13.7	270	9	BB595946	BB595946 BB595946
	25	50.8	13.7	869	10	BF540248	BF540248 602050296
	26	45	12.1	986	12	CNS076KL	AL431515 T3 end of
	27	42.2	11.3	484	10	BJ059218	BJ059218 BJ059218
c	28	42.2	11.3	687	10	BJ098508	BJ098508 BJ098508
	29	42	11.3	597	10	BJ038615	BJ038615 BJ038615
	30	40.4	10.9	589	10	BJ094875	BJ094875 BJ094875
	31	40.4	10.9	629	10	BJ095114	BJ095114 BJ095114
	32	39.8	10.7	309	10	BJ059046	BJ059046 BJ059046
c	33	38.4	10.3	634	9	AW187570	AW187570 BNLGHi777
	34	38.4	10.3	694	10	BF479357	BF479357 L48-3026T
	35	38.4	10.3	697	10	BM301804	BM301804 MCA045A01
	36	37.8	10.2	455	10	BG554741	BG554741 dac30h03.
	37	37.2	10.0	539	10	BI450048	BI450048 daa97c09.
	38	36.2	9.7	431	9	BB789522	BB789522 BB789522
c	39	36.2	9.7	772	10	BE273157	BE273157 601142325
	40	36	9.7	1393	10	BF131615	BF131615 601820422
	41	35.8	9.6	538	9	AV883212	AV883212 AV883212
	42	35.8	9.6	673	9	AV889968	AV889968 AV889968
	43	35.8	9.6	675	9	AV676222	AV676222 AV676222
	44	35.8	9.6	709	9	AV858687	AV858687 AV858687
	45	35.6	9.6	578	9	AV391303	AV391303 AV391303

ALIGNMENTS

RESULT 1
BG208163/c
LOCUS BG208163 803 bp mRNA linear EST 21-APR-2001
DEFINITION RST27654 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG208163
VERSION BG208163.1 GI:13729850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 550.
FEATURES Location/Qualifiers
source 1. .803
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

```
BASE COUNT      222 a    172 c    171 g    238 t
ORIGIN

  Query Match             96.2%;  Score 357.8;  DB 10;  Length 803;
  Best Local Similarity   99.2%;  Pred. No. 1.2e-96;
  Matches  370;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCG-AAGGATTTTTAT 59
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     688 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAAGGATTTTTAT 629

Qy      60 TACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAA 119
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     628 TACTTATATGTACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAA 569

Qy     120 AGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTT 179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 AGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTT 509

Qy     180 CTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTC 239
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     508 CTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCATGAGACGGGAACACTC 449

Qy     240 CAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAAT 299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 CAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAAT 389

Qy     300 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 CTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAA 329

Qy     360 AATGTCCCCCTGA 372
          |||||||||||||
Db     328 AATGTCCCCCTGA 316


RESULT 2
AI962650
LOCUS       AI962650                410 bp    mRNA    linear   EST 08-MAR-2000
DEFINITION  wq42e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473948 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI962650
VERSION     AI962650.1  GI:5755363
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 770   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2473948"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      120 a     93 c     93 g    104 t
ORIGIN

  Query Match             90.3%;  Score 336;  DB 9;  Length 410;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-90;
  Matches  336;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 77

Qy      97 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 137

Qy     157 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 197

Qy     217 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 257

Qy     277 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     258 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 317

Qy     337 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 372
          ||||||||||||||||||||||||||||||||||||
Db     318 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 353


RESULT 3
AI654552
LOCUS       AI654552                429 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wb48b12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2308895 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI654552
VERSION     AI654552.1  GI:4738531
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 429)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 771   Std Error: 0.00
```

```
           Seq primer: -40UP from Gibco
           High quality sequence stop: 411.
FEATURES             Location/Qualifiers
     source          1. .429
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2308895"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT      127 a    100 c     97 g    104 t      1 others
ORIGIN

  Query Match             90.3%;  Score 336;  DB 9;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-90;
  Matches  336;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      37 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCT 71

Qy      97 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 131

Qy     157 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 CTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTG 191

Qy     217 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 AAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGG 251

Qy     277 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     252 CAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAG 311

Qy     337 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 372
           ||||||||||||||||||||||||||||||||||||
Db     312 AACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 347


RESULT 4
AI339609
LOCUS       AI339609                391 bp    mRNA    linear   EST 29-DEC-1998
DEFINITION  qq42a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935156
            3' similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI339609
VERSION     AI339609.1  GI:4076536
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
```

```
           Seq primer: -40UP from Gibco
           High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1935156"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      119 a     93 c     93 g     86 t
ORIGIN

  Query Match             89.2%;  Score 331.8;  DB 9;  Length 391;
  Best Local Similarity   99.4%;  Pred. No. 5.7e-89;
  Matches  333;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      38 ACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTG 97
           |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db       3 ACGTCTTCCGAAGGATTTTTATTACTTATGGGGACAATTGGCGCCAGAACACAACAGCTG 62

Qy      98 AGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACC 157
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 AGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACC 122

Qy     158 TCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGA 217
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 TCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGA 182

Qy     218 AATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGC 277
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 AATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGC 242

Qy     278 AGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGA 337
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 AGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGA 302

Qy     338 ACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 372
           ||||||||||||||||||||||||||||||||||||
Db     303 ACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 337


RESULT 5
AI246239
LOCUS       AI246239                372 bp    mRNA    linear   EST 28-JAN-1999
DEFINITION  qi29g04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1857942
            3' similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AI246239
VERSION     AI246239.1  GI:3841636
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

```
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 921   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 365.
FEATURES              Location/Qualifiers
     source           1. .372
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1857942"
                      /clone_lib="Soares_NhHMPu_S1"
                      /tissue_type="Pooled human melanocyte, fetal heart, and
                      pregnant uterus"
                      /lab_host="DH10B"
                      /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                      (Pharmacia) with a modified polylinker; Site_1: Not I;
                      Site_2: Eco RI; Equal amounts of plasmid DNA from three
                      normalized libraries (melanocyte 2NbHM, pregnant uterus
                      NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                      were made in vitro. Following HAP purification, this DNA
                      was used as tracer in a subtractive hybridization
                      reaction. The driver was PCR-amplified cDNAs from pools of
                      5,000 clones made from the same 3 libraries. The pools
                      consisted of I.M.A.G.E. clones 260232-265223,
                      340488-345479, and 484488-489479."
BASE COUNT      115 a     89 c     86 g     82 t
ORIGIN

  Query Match             88.2%;  Score 328;  DB 9;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-88;
  Matches  328;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      45 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 60

Qy     105 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT 164
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGT 120

Qy     165 GATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 224
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 180

Qy     225 GAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAA 284
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAA 240

Qy     285 GTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGG 344
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGG 300

Qy     345 TGCGGCTGGGTTCAAAATGTCCCCCTGA 372
           ||||||||||||||||||||||||||||
Db     301 TGCGGCTGGGTTCAAAATGTCCCCCTGA 328


RESULT 6
AK008619
LOCUS       AK008619               1691 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male stomach cDNA, RIKEN full-length enriched
            library, clone:2200002I16:homolog to MINIMUM POTASSIUM ION
            CHANNEL-RELATED PEPTIDE 1 (MIRP1) (MINK-RELATED PEPTIDE 1), full
            insert sequence.
ACCESSION   AK008619
VERSION     AK008619.1  GI:12842913
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2200002I16.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 1691)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES              Location/Qualifiers
     source           1. .1691
                      /organism="Mus musculus"
```

```
                     /strain="C57BL/6J"
                     /db_xref="MGD:MGI:1901204"
                     /db_xref="taxon:10090"
                     /clone="2200002I16"
                     /sex="male"
                     /tissue_type="stomach"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             149. .520
                     /note="data source:SPTR, source key:Q9WTW0, evidence:ISS
                     homolog to MINIMUM POTASSIUM ION CHANNEL-RELATED PEPTIDE 1
                     (MIRP1) (MINK-RELATED PEPTIDE 1)
                     putative"
                     /codon_start=1
                     /protein_id="BAB25781.1"
                     /db_xref="GI:12842914"
                     /translation="MATLANLTQTLEDAFKKIFITYMDSWRRNTTAEEQALQARVDAE
                     NFYYVILYLMVMIGMFSFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQEKYKSQILH
                     LEDSKATIHENMGATGFTVSP"
     polyA_signal    1673. .1678
                     /note="putative"
     polyA_site      1691
                     /note="putative"
BASE COUNT      482 a    365 c    410 g    434 t
ORIGIN

  Query Match             72.5%;  Score 269.6;  DB 11;  Length 1691;
  Best Local Similarity   82.8%;  Pred. No. 5.4e-70;
  Matches  308;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | || ||| ||||||| || ||||| ||||| || | |||| || ||||||||||
Db    149 ATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAAAAAGATTTTTATT 208

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          |||||||||||||  ||| |   |||||| ||||| ||| |  |||| ||||| |||| |
Db    209 ACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGCACTCCAGGCCAGA 268

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| |||||||||||||| |||||||||||||||||||||||| || ||||||
Db    269 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 328

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          || |||||| | |||||||||||||||||| ||||| || ||| | || || ||||||
Db    329 TCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGAGAGCACTCC 388

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          | ||||| |||||||||||||| || || || |||||||||||||||||| || || |||
Db    389 CAGGACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTACAAAAGTCAGATC 448

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          || |||| ||||| || |||||||||||||||||||||||| || ||| | ||||||| |
Db    449 CTGCATCTGGAAGACTCCAAGGCCACCATCCATGAGAACATGGGGGCGACGGGGTTCACA 508

Qy    361 ATGTCCCCCTGA 372
          |||| ||||||
Db    509 GTGTCACCCTGA 520


RESULT 7
D85797
LOCUS       D85797                   470 bp    mRNA    linear   EST 09-SEP-1996
DEFINITION  D85797 Rat 21 day old female ovary mRNA PMSG 3h Rattus norvegicus
            cDNA, mRNA sequence.
ACCESSION   D85797
VERSION     D85797.1  GI:1469812
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 470)
  AUTHORS   Miyamoto,K., Mizutani,T., Numata,Y. and Okada,T.
  TITLE     Rat 21 day old female ovary mRNA
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Miyamoto,K.
            Institute for Molecular and Cellular Reg
            Gunma Univ., Biosignal Research Center
            Shouwa machi 3-39-15, Maebashi, Gunma 371, Japan
            Email: tmizu@sb.gunma-u.ac.jp
            5'-59.
FEATURES             Location/Qualifiers
     source          1. .470
                     /organism="Rattus norvegicus"
                     /strain="Wistar"
                     /db_xref="taxon:10116"
                     /clone_lib="Rat 21 day old female ovary mRNA PMSG 3h"
                     /sex="female"
                     /tissue_type="ovary"
                     /dev_stage="21 day old"
BASE COUNT      116 a    127 c    128 g     95 t      4 others
ORIGIN

  Query Match             70.1%;  Score 260.8;  DB 10;  Length 470;
  Best Local Similarity   80.9%;  Pred. No. 1.4e-67;
  Matches  301;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy      1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
          ||| | |||||| |||| || || ||||| ||||| || | |||| || | |||| |||
Db     37 ATGACCACTTTAGCCAACTTGACGCAGACCCTGGAGGATGCCTTCAAAAAGGTTTTCATT 96

Qy     61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
          |||||||||||||  ||| |   |||||||||||| || ||| |||| ||||| |||| |
Db     97 ACTTATATGGACAGCTGGAGGAGGAACACAACAGCCGAACAACAGGCGCTCCAGGCCAGA 156

Qy    121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
          || ||||| |||||||||||||| |||||||||||||||||||||||| || ||||||
Db    157 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 216

Qy    181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
          | |||||| | |||||||||||||||||| ||||| || ||| | ||||| ||||||
Db    217 GCCTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGGGAGCACTCC 276

Qy    241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
          | ||||| |||||||||| | | || ||||| |||||| | ||||| | ||| || |||
Db    277 CAGGACCCGTACCACCAGTNCNTCGTGGAGGATTGGCAGCAGAAGTATAGGAGTCAGATC 336

Qy    301 TTGAATCTAGAAGAATCGAAGGCCACCATCCATGAGAACATTGGTGCGGCTGGGTTCAAA 360
          | | |||| ||||| || ||||||| |||||||| ||| | || ||| | ||||||| |
Db    337 TNGCATCTGGAAGACTCCAAGGCCATCATCCATGATAACCTGGGGGCGACGGGGTTCACA 396

Qy    361 ATGTCCCCCTGA 372
          |||| ||||||
Db    397 NTGTCACCCTGA 408


RESULT 8
BG261965
LOCUS       BG261965                1003 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  602373784F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481325 5',
            mRNA sequence.
ACCESSION   BG261965
VERSION     BG261965.1  GI:12771781
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
```

```
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10316  row: g  column: 22
           High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .1003
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4481325"
                     /clone_lib="NIH_MGC_94"
                     /tissue_type="retina"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 3.3 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      249 a    218 c    302 g    234 t
ORIGIN

  Query Match             65.9%;  Score 245;  DB 10;  Length 1003;
  Best Local Similarity   81.9%;  Pred. No. 1.1e-62;
  Matches  307;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    2;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||| | || ||| ||||||| || ||||| ||||| || | ||||  || ||||||||||
Db      91 ATGGCCACATTAGCCAATTTGACCCAGACACTGGAGGATGCCTTCAAAAAGATTTTTATT 150

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  ||| |   |||||| ||||| ||| |  |||| ||||| |||| |
Db     151 ACTTATATGGACAGCTGGAGGAGGAACACGACAGCCGAGGAGCAGGCACTCCAGGCCAGA 210

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           || ||||| ||||||||||||||| ||||||||||||||||||||||||||| || ||||||
Db     211 GTGGATGCCGAGAACTTCTACTACGTCATCCTGTACCTCATGGTGATGATCGGCATGTTC 270

Qy     181 TCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAACACTCC 240
           || |||||| | |||||||||||||||||||| ||||| || ||| | || || ||||||
Db     271 TCGTTCATCGTGGTGGCCATCCTGGTGAGCACGGTGAAGTCGAAGCGGCGAGAGCACTCC 330

Qy     241 AATGACCCCTACCACCAGTACATTGTAGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           |  |||| |||||||||||||| || || || ||||||||||||||||| || || |||
Db     331 CAGCACCCGTACCACCAGTACATCGTGGAAGATTGGCAGGAAAAGTACAAAAGTCAGATC 390

Qy     301 TTGAATCTAGAAGAATCGAA--GGCCACCATCCATGAGAACAT-TGGTGCGGCTGGGTTC 357
           || |||| ||||| || ||  |||||||||||||||||||||  || ||| | ||||||
Db     391 CTGCATCTGGAAGACTCCAAAGGGCCACCATCCATGAGAACATGGGGGGCGACGGGGTTC 450

Qy     358 AAAATGTCCCCCTGA 372
           | | |||| ||||||
Db     451 ACAGTGTCACCCTGA 465


RESULT 9
BG221966
LOCUS       BG221966                 746 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST41783 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG221966
VERSION     BG221966.1  GI:13747987
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.
            , Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith
            ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 547.
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Athersys RAGE Library"
                     /cell_line="HT1080"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
BASE COUNT      241 a    138 c    123 g    243 t      1 others
ORIGIN

  Query Match             47.8%;  Score 177.8;  DB 10;  Length 746;
  Best Local Similarity   93.2%;  Pred. No. 1.5e-42;
  Matches  207;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     526 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 585

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           |||||||||||||||||||||||||||||| |||||||||| |||||||||| |||||||
Db     586 ACTTATATGGACAATTGGCGCCAGAACACACCAGCTGAGCAGGAGGCCCTCC-AGCCAAA 644

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           |||||||||||||||||||||||||||||| | |||  |||| ||||||||||||||||
Db     645 GTTGATGCTGAGAACTTCTACTATGTCATCCCGGACCCAATGGNGATGATTGGAATGTTC 704

Qy     181 TCTTTCAT-CATCGTGGCCATCCTGGTGAGCACTGTGAAATC 221
           | ||| ||  || | |||||||||||| ||||||||||||||
Db     705 TTTTTAATAAATGGGGGCCATCCTGGGGAGCACTGTGAAATC 746


RESULT 10
BG938225
LOCUS       BG938225                 351 bp    mRNA    linear   EST 11-JUN-2001
DEFINITION  1Abo14A12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
            sequence.
ACCESSION   BG938225
VERSION     BG938225.1  GI:14337597
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G.
  TITLE     cDNA's from bovine abomasum tissue
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dr. Stephen Moore
            . Beef Genomics Laboratory
            Dept of AFNS, University of Alberta
            410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
            Tel: 780 492 0169
            Fax: 780 492 4265
            Email: smoore@afns.ualberta.ca
            The sequence best matches gb:AP001719 (Homo sapiens genomic DNA,
```

chromosome 21q, section 63/105) in main database at high score of 212.0 and E-value of 9e-53
PCR PRimers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence stop: 351
POLYA=No.

```
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="Bovine Abomasum cDNA Library"
                     /sex="Two males and one female mixed"
                     /tissue_type="Gastrointestinal tissue (GIT)"
                     /cell_type="Epithelial"
                     /dev_stage="Young adult"
                     /lab_host="XL1-BlueMRF'-strain"
                     /note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
                     I; Site_2: Xho I"
BASE COUNT      104 a     89 c     76 g     82 t
ORIGIN
```

Query Match 45.2%; Score 168.2; DB 10; Length 351;
Best Local Similarity 87.1%; Pred. No. 8.4e-40;
Matches 196; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

```
Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||| | ||| |||||||| | |||||||| |||||| | ||||||  || ||||||||||
Db     127 ATGCCAACTCTATCCAATCTGACACAGACACTGGAATATGTCTTCAAAAAGATTTTTATC 186

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||| ||||| || |||| |  |||||||||  | ||||||||||||||| ||||||||
Db     187 ACTTACATGGAAAACTGGCACAGGAACACAACGGTTGAGCAAGAGGCCCTGCAAGCCAAG 246

Qy     121 GTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTC 180
           |||||||||||||||||||||||||||||| ||||||| |||||||||| |||||||||
Db     247 GTTGATGCTGAGAACTTCTACTATGTCATCTTGTACCTTATGGTGATGATCGGAATGTTC 306

Qy     181 TCTTT-CATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAA 224
           ||||| |||||| || ||||||||||||||||| ||||||||||
Db     307 TCTTTCCATCATTGTAGCCATCCTGGTGAGCACGGTGAAATCCAA 351
```

```
RESULT 11
AA633404
LOCUS       AA633404                188 bp    mRNA    linear   EST 28-OCT-1997
DEFINITION  np69h11.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1131621 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AA633404
VERSION     AA633404.1  GI:2555264
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 188)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 785   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 167.
FEATURES             Location/Qualifiers
     source          1. .188
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1131621"
                     /clone_lib="NCI_CGAP_Br2"
                     /sex="female, pooled"
                     /tissue_type="breast"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from pooled bulk
                     breast tumor tissue, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  This library is the normalized version of
                     NCI_CGAP_Br1.1. Library was constructed by Bento Soares
                     and M. Fatima Bonaldo. "
BASE COUNT       66 a     45 c     45 g     32 t
ORIGIN
```

Query Match 43.0%; Score 160; DB 9; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     213 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 60

Qy     273 CTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCA 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGGCAGGAAAAGTACAAGAGCCAAATCTTGAATCTAGAAGAATCGAAGGCCACCATCCA 120

Qy     333 TGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 372
           ||||||||||||||||||||||||||||||||||||||||
Db     121 TGAGAACATTGGTGCGGCTGGGTTCAAAATGTCCCCCTGA 160
```

```
RESULT 12
AA935321
LOCUS       AA935321                121 bp    mRNA    linear   EST 07-JUL-1998
DEFINITION  oo71g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571680 3'
            similar to SW:MINK_HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM
            CHANNEL PROTEIN ;, mRNA sequence.
ACCESSION   AA935321
VERSION     AA935321.1  GI:3092478
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 121)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 763   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
```

```
FEATURES             Location/Qualifiers
     source          1. .121
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1571680"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector.  Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       33 a     31 c     28 g     29 t
ORIGIN

  Query Match             32.1%;  Score 119.4;  DB 9;  Length 121;
  Best Local Similarity   99.2%;  Pred. No. 2.5e-25;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     153 GTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCAC 212
           ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1 GTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCAACGTGGCCATCCTGGTGAGCAC 60

Qy     213 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGAGGA 120

Qy     273 C 273
           |
Db     121 C 121


RESULT 13
AW869303/c
LOCUS       AW869303                311 bp    mRNA    linear   EST 22-MAY-2000
DEFINITION  MR3-SN0067-240400-006-f11 SN0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW869303
VERSION     AW869303.1  GI:8003356
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 311)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=MR3-SN0067-240
            400-006-f11&t3=2000-04-24&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 74.
```

```
FEATURES             Location/Qualifiers
     source          1. .311
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="SN0067"
                     /dev_stage="Adult"
                     /note="Organ: stomach_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       60 a     80 c     76 g     95 t
ORIGIN

  Query Match             26.6%;  Score 99;  DB 9;  Length 311;
  Best Local Similarity   90.7%;  Pred. No. 5.1e-19;
  Matches  117;  Conservative    0;  Mismatches   10;  Indels    2;  Gaps    1;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     182 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATC 123

Qy      61 ACTTATATGGACAATTGG--CGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCA 118
           ||| |||||||||| ||    | ||||||| |||||||||| ||||||||||||||||
Db     122 ACTCATATGGACAATCGGGCGCCGAGAACACGACAGCTGAGCGAGAGGCCCTCCAAGCCT 63

Qy     119 AAGTTGATG 127
           ||| |||||
Db      62 AAGATGATG 54


RESULT 14
BB564873
LOCUS       BB564873                314 bp    mRNA    linear   EST 29-NOV-2000
DEFINITION  BB564873 RIKEN full-length enriched, adult male stomach Mus
            musculus cDNA clone 2200002I16 5', mRNA sequence.
ACCESSION   BB564873
VERSION     BB564873.1  GI:11455765
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 314)
  AUTHORS   Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P.
            , Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
            ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
            Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
            Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A.,
            Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
            ,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
```

```
           ,Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
           system. Genome Res. 9 (5), 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
           19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
           further details.
FEATURES             Location/Qualifiers
     source          1. .314
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="2200002I16"
                     /clone_lib="RIKEN full-length enriched, adult male
                     stomach"
                     /sex="male"
                     /tissue_type="stomach"
                     /dev_stage="adult"
                     /lab_host="SOLR"
                     /note="Site_1: XhoI; Site_2: SstI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with XhoI and SstI."
BASE COUNT       98 a     77 c     74 g     65 t
ORIGIN

  Query Match             24.2%;  Score 90;  DB 9;  Length 314;
  Best Local Similarity   76.0%;  Pred. No. 2.6e-16;
  Matches  111;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
             ||| | || ||| ||||||| || || || ||||| || | ||||  ||  |||||||||
Db     149 ATGGCCACATTAGCCAATTTGACCCAAACACTGGAGGATGCCTTCAAAAAAATTTTTATT 208

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAA 120
           ||||||||||||  |||     ||||||||||  |  || |  |||| ||||||||||||
Db     209 ACTTATATGGACAGCTGGAAGAGGAACACAACATCCAAGGAGCAGGCACTCCAAGCCAAA 268

Qy     121 GTTGATGCTGAGAACTTCTACTATGT 146
           || || ||  |||| ||||||||  ||
Db     269 GTGGAAGCCAAGAATTTCTACTAGGT 294


RESULT 15
BB574249
LOCUS       BB574249                272 bp    mRNA    linear   EST 30-NOV-2000
DEFINITION  BB574249 RIKEN full-length enriched, 11 days pregnant adult female
            ovary and uterus Mus musculus cDNA clone 5031401M02, mRNA sequence.
ACCESSION   BB574249
VERSION     BB574249.1  GI:11470793
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 272)
  AUTHORS   Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P.
            , Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno
            ,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K.,
            Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C.,
            Sakai,K., Sasaki,D., Sato,K., Shibata,K., Shibata,Y., Shinagawa,A.,
            Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Tanaka
            ,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshiki,A., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Aizawa,K. et al. 2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
            Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .272
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="5031401M02"
                     /clone_lib="RIKEN full-length enriched, 11 days pregnant
                     adult female ovary and uterus"
                     /sex="female"
                     /tissue_type="ovary and uterus"
                     /dev_stage="11 days pregnant, adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI."
BASE COUNT       87 a     56 c     66 g     63 t
ORIGIN

  Query Match             15.5%;  Score 57.6;  DB 9;  Length 272;
  Best Local Similarity   72.1%;  Pred. No. 1.4e-06;
  Matches   75;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       1 ATGTCTACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATT 60
             ||| | ||||||||||||||| |  ||||| ||| |||| | |||| |||  |||||||||
Db     169 ATGGCCACTTTATCCAATTTAATCCAGACACTGAAAGATGCCTTCTGAATTATTTTTATT 228

Qy      61 ACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA 104
           |||||  |||| | |||| |   ||| |  | ||   || | ||
Db     229 ACTTAGGTGGAGAGTTGGAGGAGGAAGAGTAAAGGCAAGGAGGA 272
```

Search completed: October 24, 2002, 14:17:22
Job time : 1610 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 21, 2003, 20:14:00 ; Search time 21.4496 Seconds
(without alignments)
5275.799 Million cell updates/sec

Title: US-09-550-163-1_COPY_74_442
Perfect score: 369
Sequence: 1 atgtctactttatccaatttt.....ctgggttcaaaatgtccccc 369

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	53.2	14.4	398	1	US-08-118-101A-5	Sequence 5, Appli
	2	53.2	14.4	436	4	US-09-679-185-1	Sequence 1, Appli
	3	53.2	14.4	1703	3	US-09-135-021-77	Sequence 77, Appl
	4	53.2	14.4	1703	4	US-09-135-020-3	Sequence 3, Appli
	5	53.2	14.4	1703	4	US-09-135-010A-3	Sequence 3, Appli
	6	53.2	14.4	1703	4	US-09-444-871-3	Sequence 3, Appli
	7	53.2	14.4	1703	4	US-09-597-735-3	Sequence 3, Appli
	8	53.2	14.4	1703	4	US-09-444-295-3	Sequence 3, Appli
	9	53.2	14.4	1703	4	US-09-597-732-3	Sequence 3, Appli
	10	51.6	14.0	436	4	US-09-679-185-3	Sequence 3, Appli
	11	36.6	9.9	2652	1	US-08-318-831-1	Sequence 1, Appli
	12	36	9.8	1380	1	US-08-110-286A-1	Sequence 1, Appli
	13	36	9.8	1495	4	US-08-482-746-1	Sequence 1, Appli
	14	36	9.8	1582	4	US-08-482-746-14	Sequence 14, Appl
	15	33.6	9.1	645	3	US-09-069-896-2	Sequence 2, Appli
	16	33.6	9.1	645	4	US-09-471-468-2	Sequence 2, Appli
	17	33	8.9	606	4	US-09-328-111-133	Sequence 133, App
c	18	33	8.9	2912	4	US-09-307-143-3	Sequence 3, Appli
c	19	32.4	8.8	837	4	US-08-998-416-303	Sequence 303, App
c	20	32.4	8.8	4659	4	US-09-221-017B-823	Sequence 823, App
	21	30.6	8.3	6822	4	US-09-426-998-3	Sequence 3, Appli
	22	30.6	8.3	7741	4	US-09-426-998-4	Sequence 4, Appli
c	23	30.4	8.2	28473	4	US-08-961-527-83	Sequence 83, Appl
	24	30.2	8.2	33000	4	US-09-215-694-18	Sequence 18, Appl
c	25	29.8	8.1	2266	2	US-08-724-394A-18	Sequence 18, Appl
	26	29.8	8.1	246240	2	US-08-724-394A-20	Sequence 20, Appl
	27	29.8	8.1	246240	2	US-08-724-394A-21	Sequence 21, Appl
	28	29.8	8.1	246240	2	US-08-724-394A-22	Sequence 22, Appl
	29	29.6	8.0	462	3	US-08-863-813A-33	Sequence 33, Appl
	30	29.6	8.0	3273	6	5516630-1	Patent No. 5516630
c	31	29.6	8.0	6002	4	US-09-345-882-4	Sequence 4, Appli
	32	29.6	8.0	7486	3	US-08-475-886-5	Sequence 5, Appli
	33	29.6	8.0	7486	4	US-08-397-232-3	Sequence 3, Appli
	34	29.6	8.0	7486	4	US-09-653-499-5	Sequence 5, Appli
	35	29.6	8.0	7488	3	US-08-475-886-3	Sequence 3, Appli
	36	29.6	8.0	7488	4	US-09-653-499-3	Sequence 3, Appli
	37	29.6	8.0	7493	3	US-08-475-886-1	Sequence 1, Appli
	38	29.6	8.0	7493	4	US-08-397-232-1	Sequence 1, Appli
	39	29.6	8.0	7493	4	US-09-171-387-1	Sequence 1, Appli
	40	29.6	8.0	7493	4	US-09-653-499-1	Sequence 1, Appli
	41	29.4	8.0	1666	4	US-09-221-017B-933	Sequence 933, App
	42	29.4	8.0	3947	4	US-08-975-762-47	Sequence 47, Appl
	43	29.4	8.0	3947	4	US-09-295-028-47	Sequence 47, Appl
	44	29.4	8.0	3947	4	US-09-106-582-47	Sequence 47, Appl
c	45	29.2	7.9	352	4	US-09-605-785-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-08-118-101A-5
; Sequence 5, Application US/08118101A
; Patent No. 5620892
; GENERAL INFORMATION:
; APPLICANT: Kurtz, Stephen E.
; APPLICANT: Knickerbocker, Aron M.
; APPLICANT: McCullough, John R.
; TITLE OF INVENTION: A STRAIN OF SACCHAROMYCES CEREVISIAE
; TITLE OF INVENTION: EXPRESSING THE GENE ENCODING POTASSIUM TRANSPORTER MINK
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,101A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..398
US-08-118-101A-5

Query Match 14.4%; Score 53.2; DB 1; Length 398;
Best Local Similarity 63.6%; Pred. No. 1.7e-08;
Matches 98; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

```
Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     141 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 200

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     201 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 260

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db     261 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 294


RESULT 2
US-09-679-185-1
; Sequence 1, Application US/09679185
; Patent No. 6458542
; GENERAL INFORMATION:
;  APPLICANT: George Jr., Alfred L.
;  APPLICANT:  Roden, Dan M
;  TITLE OF INVENTION: METHOD OF SCREENING FOR SUSCEPTIBILITY TO
;  TITLE OF INVENTION:  DRUG-INDUCED CARDIAC ARRYTHMIA
;  FILE REFERENCE: Attorney Docket No. 6458542 1242-33-2
;  CURRENT APPLICATION NUMBER: US/09/679,185
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 60/158,696
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(418)
;  PUBLICATION INFORMATION:
;   JOURNAL: Biochem. Biophys. Res. Commun.
;   VOLUME: 161
;   PAGES: 176-181
;   DATE: May-1989
;   DATABASE ACCESSION NUMBER: GenBank M26685
;   DATABASE ENTRY DATE: 1994-03-30
US-09-679-185-1

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 436;
  Best Local Similarity   63.6%;  Pred. No. 1.8e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     160 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 219

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     220 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 279

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db     280 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 313


RESULT 3
US-09-135-021-77
; Sequence 77, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-021-77

  Query Match             14.4%;  Score 53.2;  DB 3;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 4
US-09-135-020-3
; Sequence 3, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/135,020
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-020-3

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383
```

```
Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 5
US-09-135-010A-3
; Sequence 3, Application US/09135010A
; Patent No. 6277978
; GENERAL INFORMATION:
;  APPLICANT:  Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION:  KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE:  2323-133
;  CURRENT APPLICATION NUMBER: US/09/135,010A
;  CURRENT FILING DATE:  1998-08-17
;  PRIOR APPLICATION NUMBER:  60/094,477
;  PRIOR FILING DATE:  1998-07-29
;  PRIOR APPLICATION NUMBER:  08/921,068
;  PRIOR FILING DATE:  1997-08-29
;  PRIOR APPLICATION NUMBER:  08/739,383
;  PRIOR FILING DATE:  1996-10-29
;  PRIOR APPLICATION NUMBER:  60/019,014
;  PRIOR FILING DATE:  1995-12-22
;  NUMBER OF SEQ ID NOS:  116
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-135-010A-3

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 6
US-09-444-871-3
; Sequence 3, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION: KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,871
;  CURRENT FILING DATE: 1999-11-22
;  EARLIER APPLICATION NUMBER: US 09/135,020
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-444-871-3

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy    150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
          ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db    324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy    210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
          |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db    384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy    267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db    444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 7
US-09-597-735-3
; Sequence 3, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT: Sanguinetti, Michael C.
;  APPLICANT: Curran, Mark E.
;  APPLICANT: Landes, Gregory M.
;  APPLICANT: Connors, Timothy D.
;  APPLICANT: Burn, Timothy C.
;  APPLICANT: Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,735
;  CURRENT FILING DATE: 2000-06-19
;  EARLIER APPLICATION NUMBER: 09/135,010
;  EARLIER FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  EARLIER APPLICATION NUMBER: 08/921,068
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 08/739,383
;  EARLIER FILING DATE: 1996-10-29
;  EARLIER APPLICATION NUMBER: 60/019,014
;  EARLIER FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

```
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-597-735-3

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 8
US-09-444-295-3
; Sequence 3, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
;  TITLE OF INVENTION:  CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
;  TITLE OF INVENTION:  KCNE1 AS AN LQT GENE
;  FILE REFERENCE: 2323-131
;  CURRENT APPLICATION NUMBER: US/09/444,295
;  CURRENT FILING DATE:  1999-11-22
;  PRIOR APPLICATION NUMBER: 09/135,020
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-444-295-3

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 9
US-09-597-732-3
; Sequence 3, Application US/09597732
; Patent No. 6451534
; GENERAL INFORMATION:
;  APPLICANT: Keating, Mark T.
;  APPLICANT:  Sanguinetti, Michael C.
;  APPLICANT:  Curran, Mark E.
;  APPLICANT:  Landes, Gregory M.
;  APPLICANT:  Connors, Timothy D.
;  APPLICANT:  Burn, Timothy C.
;  APPLICANT:  Splawski, Igor
;  TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
;  FILE REFERENCE: 2323-133
;  CURRENT APPLICATION NUMBER: US/09/597,732
;  CURRENT FILING DATE:  2000-06-19
;  PRIOR APPLICATION NUMBER: 09/135,010
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 60/094,477
;  PRIOR FILING DATE: 1998-07-29
;  PRIOR APPLICATION NUMBER: 08/921,068
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 08/739,383
;  PRIOR FILING DATE: 1996-10-29
;  PRIOR APPLICATION NUMBER: 60/019,014
;  PRIOR FILING DATE: 1995-12-22
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1703
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (193)..(579)
US-09-597-732-3

  Query Match             14.4%;  Score 53.2;  DB 4;  Length 1703;
  Best Local Similarity   63.6%;  Pred. No. 3.9e-08;
  Matches   98;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     324 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 383

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     384 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 443

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
           || | |||||| || ||| |||||  | |  ||
Db     444 CGATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 477


RESULT 10
US-09-679-185-3
; Sequence 3, Application US/09679185
; Patent No. 6458542
; GENERAL INFORMATION:
;  APPLICANT: George Jr., Alfred L.
;  APPLICANT:  Roden, Dan M
;  TITLE OF INVENTION: METHOD OF SCREENING FOR SUSCEPTIBILITY TO
;  TITLE OF INVENTION:  DRUG-INDUCED CARDIAC ARRYTHMIA
;  FILE REFERENCE: Attorney Docket No. 6458542 1242-33-2
;  CURRENT APPLICATION NUMBER: US/09/679,185
;  CURRENT FILING DATE:  2000-10-04
;  PRIOR APPLICATION NUMBER: 60/158,696
;  PRIOR FILING DATE: 1999-10-08
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 436
```

```
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (29)..(418)
US-09-679-185-3

  Query Match             14.0%;  Score 51.6;  DB 4;  Length 436;
  Best Local Similarity   63.0%;  Pred. No. 6.2e-08;
  Matches   97;  Conservative    0;  Mismatches   54;  Indels    3;  Gaps    1;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           ||| ||| || |  || |  | ||| | |||   ||| ||| | ||| |||| || ||||
Db     160 CCTCTACGTCCTCATGGTACTGGGATTCTTCGGCTTCTTCACCCTGGGCATCATGCTGAG 219

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTG---T 266
           |    |    |||||||  | ||| ||||| || ||||| | | ||   ||||| |
Db     220 CTACATCCGCTCCAAGAAGCTGGAGCACTCGAACGACCCATTCAACGTCTACATCGAGTC 279

Qy     267 AGAGGACTGGCAGGAAAAGTACAAGAGCCAAATC 300
             | | |||||| || ||| |||||  | |  ||
Db     280 CAATGCCTGGCAAGAGAAGGACAAGGCCTATGTC 313


RESULT 11
US-08-318-831-1
; Sequence 1, Application US/08318831
; Patent No. 5656595
;  GENERAL INFORMATION:
;    APPLICANT:  Schweighoffer, Fabien
;    APPLICANT:  Tocque, Bruno
;    TITLE OF INVENTION:  PEPTIDES HAVING A GDP EXCHANGE FACTOR
;    TITLE OF INVENTION:  ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SAID PEPTIDES,
;    TITLE OF INVENTION:  PREPARATION AND UTILIZATION
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.1 (EPO Patentin)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,831
;      FILING DATE:  19 October 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR92/04827
;      FILING DATE:  21-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, Julie K.
;      REGISTRATION NUMBER:  P-38,619
;      REFERENCE/DOCKET NUMBER:  ST92033-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2652 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2445
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  445..2445 (SEQ ID NO 3)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  976..2445 (SEQ ID NO 4)
US-08-318-831-1

  Query Match              9.9%;  Score 36.6;  DB 1;  Length 2652;
  Best Local Similarity   53.1%;  Pred. No. 0.022;
  Matches   78;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy      55 TTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAA 114
           | ||  | |  | |   | | | |  ||| ||| |  || ||||    | | ||  || |
Db    2402 TCTACGAGTCTTCTCTCCGAATAGAACCAAAACTCCCCACCTGAAGCTGTGCCCAGCCCA 2461

Qy     115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
           | |  || || | | | | || | | |||  | || ||||||  |  | ||   | ||
Db    2462 GACCCAGCTGCTCCCGGGGACATGTGCTAGATGATACTGTACATATTCGTTTGGTTTCAC 2521

Qy     175 ATGTTCTCTTTCATCATCGTGGCCATC 201
             | | |  ||| |||   ||  | ||
Db    2522 TGGATTTTCTTCTTCAGTATGTGCTTC 2548


RESULT 12
US-08-110-286A-1
; Sequence 1, Application US/08110286A
; Patent No. 5728545
;  GENERAL INFORMATION:
;    APPLICANT:  Perrin, Marilyn H.
;    APPLICANT:  Chen, Ruoping
;    APPLICANT:  Lewis, Kathy A.
;    APPLICANT:  Vale Jr., Wylie W.
;    APPLICANT:  Donaldson, Cynthia J.
;    TITLE OF INVENTION:  CLONING AND RECOMBINANT PRODUCTION OF
;    TITLE OF INVENTION:  CRF RECEPTOR(S)
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pretty, Schroeder, Brueggemann & Clark
;      STREET:  444 South Flower Street, Suite 2000
;      CITY:  Los Angeles
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/110,286A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/079,320
;      FILING DATE:  18-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter, Stephen E.
;      REGISTRATION NUMBER:  31,192
;      REFERENCE/DOCKET NUMBER:  P41 9439
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-546-4737
;      TELEFAX:  619-546-9392
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1380 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
```

```
;       LOCATION:  82..1329
;       OTHER INFORMATION:  /product= "HUMAN PITUITARY
;       OTHER INFORMATION:  CRF-RECEPTOR"
;       OTHER INFORMATION:  /note= "This sequence is encoded by clone
;       OTHER INFORMATION:  "CRF-R1"."
US-08-110-286A-1

  Query Match             9.8%;  Score 36;  DB 1;  Length 1380;
  Best Local Similarity   52.7%;  Pred. No. 0.025;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     862 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 921

Qy     175 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 234
             || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db     922 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 981

Qy     235 CACTCCAATGACCCCTACCACCAGTACA 262
           | |||          |   |||||||
Db     982 TCCACCACGTCTGAGACCATTCAGTACA 1009


RESULT 13
US-08-482-746-1
; Sequence 1, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
;  APPLICANT: Perrin, Marilyn H.
;  APPLICANT: Chen, Ruoping
;  APPLICANT: Lewis, Kathy A.
;  APPLICANT: Vale Jr., Wylie W.
;  APPLICANT: Donaldson, Cynthia J.
;  APPLICANT: Sawchenko, Paul
;  TITLE OF INVENTION: Cloning and Recombinant Production of
;  TITLE OF INVENTION: CRF Receptor(s)
;  FILE REFERENCE: P41-90002
;  CURRENT APPLICATION NUMBER: US/08/482,746B
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: US 08/374,009
;  EARLIER FILING DATE: 1995-01-17
;  EARLIER APPLICATION NUMBER: US 08/353,537
;  EARLIER FILING DATE: 1994-12-09
;  EARLIER APPLICATION NUMBER: PCT/US94/05908
;  EARLIER FILING DATE: 1994-05-25
;  EARLIER APPLICATION NUMBER: US 08/110,286
;  EARLIER FILING DATE: 1993-08-23
;  EARLIER APPLICATION NUMBER: US 08/079,320
;  EARLIER FILING DATE: 1993-06-18
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (82)...(1326)
;   OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
;   OTHER INFORMATION: /note= "This sequence is encoded by clone
;   OTHER INFORMATION: "CRF-R1"."
US-08-482-746-1

  Query Match             9.8%;  Score 36;  DB 4;  Length 1495;
  Best Local Similarity   52.7%;  Pred. No. 0.026;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     862 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 921

Qy     175 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 234
             || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db     922 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 981

Qy     235 CACTCCAATGACCCCTACCACCAGTACA 262
           | |||          |   |||||||
Db     982 TCCACCACGTCTGAGACCATTCAGTACA 1009


RESULT 14
US-08-482-746-14
; Sequence 14, Application US/08482746B
; Patent No. 6399315
; GENERAL INFORMATION:
;  APPLICANT: Perrin, Marilyn H.
;  APPLICANT: Chen, Ruoping
;  APPLICANT: Lewis, Kathy A.
;  APPLICANT: Vale Jr., Wylie W.
;  APPLICANT: Donaldson, Cynthia J.
;  APPLICANT: Sawchenko, Paul
;  TITLE OF INVENTION: Cloning and Recombinant Production of
;  TITLE OF INVENTION: CRF Receptor(s)
;  FILE REFERENCE: P41-90002
;  CURRENT APPLICATION NUMBER: US/08/482,746B
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: US 08/374,009
;  EARLIER FILING DATE: 1995-01-17
;  EARLIER APPLICATION NUMBER: US 08/353,537
;  EARLIER FILING DATE: 1994-12-09
;  EARLIER APPLICATION NUMBER: PCT/US94/05908
;  EARLIER FILING DATE: 1994-05-25
;  EARLIER APPLICATION NUMBER: US 08/110,286
;  EARLIER FILING DATE: 1993-08-23
;  EARLIER APPLICATION NUMBER: US 08/079,320
;  EARLIER FILING DATE: 1993-06-18
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH: 1582
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (82)...(1413)
;   OTHER INFORMATION: CRF-R splice-variant insert fragment inserted
;   OTHER INFORMATION: between  nucleotides 516-517 of SEQ ID NO:1.
;   OTHER INFORMATION: /note= "This sequence is contained in clone
;   OTHER INFORMATION: "CRF-R2"."
US-08-482-746-14

  Query Match             9.8%;  Score 36;  DB 4;  Length 1582;
  Best Local Similarity   52.7%;  Pred. No. 0.027;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy     115 GCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGA 174
           | ||||     ||  | | ||  | ||||  ||  || |  || |||| |  || |
Db     949 GGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTG 1008

Qy     175 ATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAGCACTGTGAAATCCAAGAGACGGGAA 234
             || ||  ||||||| || |   || | | ||  |||   | |   |||||   |||| |
Db    1009 CTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCA 1068

Qy     235 CACTCCAATGACCCCTACCACCAGTACA 262
           | |||          |   |||||||
Db    1069 TCCACCACGTCTGAGACCATTCAGTACA 1096


RESULT 15
US-09-069-896-2
; Sequence 2, Application US/09069896
; Patent No. 6071720
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Patterson, Chandra
```

```
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  DELAYED RECTIFIER POTASSIUM
;    TITLE OF INVENTION:  CHANNEL HOMOLOG
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,896
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0507 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  645 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  BRSTNOT03
;      CLONE:  637471
US-09-069-896-2

  Query Match             9.1%;  Score 33.6;  DB 3;  Length 645;
  Best Local Similarity   53.9%;  Pred. No. 0.1;
  Matches   69;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy     150 CCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTCATCATCGTGGCCATCCTGGTGAG 209
           | | ||| |  ||||  | ||     | | |    |  || |  | |  ||| || || |
Db     200 CTTCTACATTCTGGTTGTCATGTCCTTCTACGGCATTTTCTTGATCGGAATCATGCTGGG 259

Qy     210 CACTGTGAAATCCAAGAGACGGGAACACTCCAATGACCCCTACCACCAGTACATTGTAGA 269
           |    |||||||||||||| |||||  |         || |   |  | |||||  |  ||
Db     260 CTACATGAAATCCAAGAGGCGGGAGAAGAAGTCCAGCCTCCTGCTGCTGTACAAAGACGA 319

Qy     270 GGACTGGC 277
           |||  |||
Db     320 GGAGCGGC 327


Search completed: May 21, 2003, 21:39:37
Job time : 27.4496 secs
```